



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number 1063

TO: Mark Navarro
Location: cm1/8A15
Art Unit: 1645
Monday, August 18, 2003

Case Serial Number: 09/904603

From: Barb O'Bryen
Location: Biotech-Chem Library
CM1-6A05
Phone: 308-4291

barbara.obryen@uspto.gov

Search Notes

O'Bryen, Barbara

From: Navarro, Albert
Sent: Wednesday, August 06, 2003 4:23 PM
To: O'Bryen, Barbara
Subject: 09/904,603

Mark Navarro
1645
306-3225
8A15

Hello Barb,

Could I trouble you for a search and an interference search of:

SEQ ID NO: 1-2

Thanks

Mark

2/24/97

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STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library 9th - Circ Desk



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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 15, 2003, 06:52:34 ; Search time 2454 Seconds
(without alignments)
10669.177 Million cell updates/sec

Title: US-09-904-603-2

Perfect score: 640
Sequence: 1 CTCGCCGAGCGCGAGCGGCC.....GCCGCCCTAGTCAGAGGCGCA 640

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBankl: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_ov: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
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11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_com: *
21: em_or: *
22: em_ov: *
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24: em_ph: *
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27: em_sts: *
28: em_un: *
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31: em_htg_inv: *
32: em_htg_other: *
33: em_htg_mus: *
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35: em_htg_rtd: *
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37: em_htg_vrl: *
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40: em_htgo_mus: *
41: em_htgo_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	640	100.0	640	6	AR075096
2	640	100.0	640	6	AR165494
3	627.4	98.0	1030	9	AF276658
4	590.4	92.2	932	9	BC015810
5	552.4	86.3	912	9	HSMB05144
6	435.2	68.0	984	10	BC010596
7	364	55.9	366	9	BT007452
8	297.8	46.5	1029	6	AX740487
9	296.2	46.3	15795	9	HSX446K17
10	240.6	37.6	984	10	AF255953
11	240.2	37.5	66877	2	AC116062
12	239	37.3	190843	2	AC103943
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17	234.2	36.6	233682	2	AC096481
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19	231	36.1	267290	2	AC134441
20	226.4	35.4	208868	2	AC124663
21	217.6	34.0	230614	10	AL626772
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24	215	33.6	791	6	BD019774
25	215	33.6	791	6	BD094712
26	215	33.6	1937	9	AF183417
27	215	33.6	2110	9	AF303888
28	215	33.6	2151	9	BC018634
29	215	33.6	2155	9	AK025556
30	215	33.6	2157	9	AF087871
31	214.4	33.5	2159	6	AR260446
32	213.4	33.3	151111	9	AC125603
33	213.4	33.3	172393	2	AC025740
34	213.4	33.3	210933	2	AC027344
35	213.2	33.3	1805	5	BC049313
36	210.6	32.9	2073	9	HSMB05336
37	201	31.4	465	6	BD11090
38	193	30.2	164047	10	AL69413
39	192.4	30.1	537	6	AX401525
40	191	29.8	2800	14	PT080885
41	178.8	27.9	269375	2	AC114457
42	174.2	27.2	318	5	CHRCDNA1AR
43	174.2	27.2	1181	9	AF276659
44	171	26.7	204150	2	AC140656
45	169.6	26.5	242177	2	AC120179

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES
AR075096	Sequence 2 from patent US 5955312.	AR075096	AR075096.1	GI:10001848	Unknown.	Unknown.	Unclassified.	1 (bases 1 to 640)	Hillman, J.L. and Goll, S.K.	DNA encoding a novel microtubule-associated protein	Patent: US 5955312-A 21-SEP-1999;	Location/Qualifiers

Pred. No. is the number of results predicted by chance to have a

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BASE COUNT 121 a 225 c 199 g 95 t
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Best Local Similarity 100.0%; Pred. No. 1e-97;
Matches 640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 CTCCGCGAGCCGCGCGCTGCTCAGCCGAGCCCGGAGCCCTTAGCGCGAGCGC 60
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61 GGAGCCCCGGAGCCCCCAACCGAGACATCCCGCGGCCAGAGCCCGGCTGGCG 120
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421 CATCGCGGACATCTACAGAGCGAGAAAGAGAGAGCGGCTTCTATATGCTCTACGC 480
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481 CTCCAGAGAAACCTTGGCTCTGAGCCAGAGTAGGGGGGCTGGCGCTGGAGATCGGG 540
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RESULT 2
ARI65393
LOCUS ARI65393 640 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 2 from patent US 6280733.
ACCESSION ARI65393
VERSION ARI65393.1 GI:16240256
KEYWORDS
ORGANISM Unknown.
SOURCE Unknown.
REFERENCE 1 (bases 1 to 640)
AUTHORS Hillman,J.L. and Goli,S.K.
TITLE Microtubule-associated protein
JOURNAL Patent: US 6280733-A 2 28-AUG-2001;
FEATURES
source 1..640
/organism="unknown"
BASE COUNT 121 a 225 c 199 g 95 t
ORIGIN

Query Match 100.0%; Score 640; DB 6; Length 640;
Best Local Similarity 100.0%; Pred. No. 1e-97;
Matches 640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTCCGCGAGCCGCGCGCTGCTCAGCCGAGCCCGGAGCCCTTAGCGCGAGCGC 60
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61 GGAGCCCCGGAGCCCCCAACCGAGACATCCCGCGGCCAGAGCCCGGCTGGCG 120
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121 GCCCAGCCGGGCGCGCGGATGCCCTCAGACCGGCTTTCAAGCAGCGCGGAGCTTGGC 180
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RESULT 3
AF276658
LOCUS AF276658 1030 bp mRNA linear PRI 16-APR-2001
DEFINITION Homo sapiens MAP1 light chain 3-like protein 1 mRNA, complete cds.
ACCESSION AF276658
VERSION AF276658.1 GI:13625770
KEYWORDS
ORGANISM Homo sapiens (human)
SOURCE Homo sapiens
REFERENCE 1 (bases 1 to 1030)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
JOURNAL Submitted (09-JUN-2000) Institute of Genetics, Fudan University,
No. 220 Handan Road, Shanghai 200433, P.R. China
FEATURES
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155..520
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/translation="MPSDRPFKORRSFADRKKEVOQIDQHPKIPVIEYKKEKOL
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polya_signal
941..946
BASE COUNT 223 a 339 c 291 g 177 t
ORIGIN

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Best Local Similarity 99.7%; Pred.No.1.2e-95;
Matches 639; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 CTCGCCGACGCCGACGCCGCTGCTGACGCGGAGCCCGGAGACCTTAGCGCGAGGGCGC 60
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QY 61 GGAG-CCCCGGAGCCCCCAAAACCGGACACATCCCCGGCCGACAGCCCGGCGCTGCG 119
DB 75 GGAGCCCCGGAGCCCCCAAAACCGGACACATCCCCGGCCGACAGCCCGGCGCTGCG 134
QY 120 CGCCGACGCCGCGCGCGGATGCCCTCAGACCGGCGCTTTGACGAGCGGCGGAGCTTGG 179
DB 135 CGCCGACGCCGCGCGCGGCGGATGCCCTCAGACCGGCGCTTTGACGAGCGGCGGAGCTTGG 194
QY 180 CCGACCGCTGTAAAGAGGTACAGCAGATCCCGGACGACCCCGGACCAAAATCCCGGTGA 239
DB 195 CCGACCGCTGTAAAGAGGTACAGCAGATCCCGGACGACCCCGGACCAAAATCCCGGTGA 254
QY 240 TCATGACGCGGTACAAAGGTTGAGAAAGCAGCTGCCGCTCTGGACAGACCAAGTTTGG 299
DB 255 TCATGACGCGGTACAAAGGTTGAGAAAGCAGCTGCCGCTCTGGACAGACCAAGTTTGG 314
QY 300 TCCCGAGCATGTCAACATGACGCGAGTTGTCAAGATCATCCGGCGCGCTGCACTGA 359
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QY 360 ACCCCAGCCAGGCTTCTCTGCTGCTGGTGAACACAGACAGATGTGAGTGTGTCACGC 419
DB 375 ACCCCAGCCAGGCTTCTCTGCTGCTGGTGAACACAGACAGATGTGAGTGTGTCACGC 434
QY 420 CCATGCGCGACATCTACGAGCAGGAGAAAGACGAGCGGCTTCTCTATATATGCTCTAC 479
DB 435 CCATGCGCGACATCTACGAGCAGGAGAAAGACGAGCGGCTTCTCTATATATGCTCTAC 494
QY 480 CCTCCGAGAAACCTTCGGCTTCTGAGCCAGCAGTAGGGGGGCTCGGCTTGGAGTTCGG 539
DB 495 CCTCCGAGAAACCTTCGGCTTCTGAGCCAGCAGTAGGGGGGCTCGGCTTGGAGTTCGG 554
QY 540 GGGCCCCGCTAGGCGCTTCCGACAGAGCTTCTGTTGCTGAACTGAGCTGCTTACCG 599
DB 555 GGGCCCCGCTAGGCGCTTCCGACAGAGCTTCTGTTGCTGAACTGAGCTGCTTACCG 614
QY 600 TGGTGCGCTGGCAGAGCATGTGCCCCCTAGTCAGAGGCA 640
DB 615 TGGTGCGCTGGCAGAGCATGTGCCCCCTAGTCAGAGGCA 655

RESULT 4
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LOCUS Homo sapiens, MAP1 light chain 3p-like protein 1, clone MGC:9521
DEFINITION IMAGE:3909192, mRNA, complete cds.
ACCESSION BC015810
VERSION BC015810.1 GI:16041838
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 932)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (09-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabbs-tr@mail.nih.gov
Tissue Procurement: AFCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LUN1)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chin, Chris Fjell, Erin Garland, Ken Gelin,
Leticia Hsiao, Martin Krzywinski, Keta Kutsche, Oliver Lee, Sue
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Diane Smalios, Michael Smith, Lorraine Spence, Jeff Stout,
Michael Thorne, Miranada Tsai, Natasha van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Zarrin.

FEATURES
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Location/Qualifiers
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CDS

BASE COUNT 178 a 315 c 275 g 163 t
ORIGIN

Query Match 92.2%; Score 590.4; DB 9; Length 942;
Best Local Similarity 99.7%; Pred.No.1.9e-89;
Matches 602; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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DB 1 CGAGCCCTTAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 60
QY 97 GCGGCCGAGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 156
DB 61 GCGGCCGAGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 120
QY 157 TTTCAGCAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 216
DB 121 TTTCAGCAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 189
QY 217 GCAGCCGAGCAAAATCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAG 276
DB 181 GCAGCCGAGCAAAATCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAG 240
QY 277 CTTGGACAAAGCGCAAGTTTTCGACCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAG 336

Db	241	CCTGACAAAGACCAAGTTTGTGGTCCGGACCATGTCAACATGACGAGATTTGGTCAAGT	300
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Db	301	CATCCGGGGCCCGCCCTTGCAGCTBAACCCACGGCAGGCGCTTCTTCGTCGTGTAAACACAGA	360
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OY	457	CGGCTTCTCTATATAGGCTTACAGCCTCCACGAAACCTTCCGCTTCTGAGCCAGCAGTAG	516
Db	421	CGGCTTCTCTATATAGGCTTACAGCCTCCACGAAACCTTCCGCTTCTGAGCCAGCAGTAG	480
OY	517	GGGGGCTCGAGCTGGAGTCCGGGGGGCCCCGGTCAAGGCGCTGCCAGAGAGCTTGGTT	576
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OY	577	CCTGAAGTGAAGCTGCTCTTACCCGTTGGTGGGCTGGGACAGGCAATGTCCCCCTTATGTCAGAG	636
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OY	637	GGCA	
Db	601	GGCA	

RESULT 5	
HSMB05143	
LOCUS	
DEFINITION	912 bp mRNA linear PRI 12-JUL-2007
	HSM805143 Homo sapiens mRNA; cDNA DKFZp761L0515 (from clone DKFZp761L0515); complete cds.
ACCESSION	
	sequence

VERSION	AL8333855.1	GI:21739336
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 912)	Ansojge, W., Wirtner, U., Mewes, H.W., Well, B. and Wiemann, S.	Direct Submission	Submitted (10-JUL-2002)	GSF, Institut fuer Bioinformatik MIPS, Ingolstaedter Landstr. 1, 85764 Neuberg, Germany
				Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

German Genome Project. This clone (DKRzp/61L0515) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clonerzpd.de Further information about the clone and the sequencing project is available at <http://mmps.gsi.de/proj/cDNA/>.

FEATURES	Location/Qualifiers
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/chromosome="20"
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/clone_id="761 (synonym:
DH10B; sites Nott + Sall"
/dev_strage="adult"
1.:912
/gene="DKFZp761L0515"
66.:431
gene
CDS

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ORIGIN				

Query March	86.3%;	Score 552.4;	DB 9;	Length 912;
Best Local Similarity	99.6%;	Pred. No. 4.5e-83;		
Matches 564;	Conservative 0;	Mismatches 1;	Indels 1;	Gaps 1

Db

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[illegible]

QY 195 AGGTACAGCAGATCCCGCACCAGCAGCCCGCAGCAAAATCCCGGTGATCATCGAGCGCTACA 254

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315 ACATGAGCGAGTTGTCAGATCATCCGGCGCGCCCTGCAGCTGAACCCCAAGCAGCCT 374

375 TCCTCCTGCTGGTGAACACAGACAGCATGAGAGTGTCTCCACGCGCCATCGCGGACATCT 434

DB 301 TCTTCCCTGCTGGTGAACACGACACAGCATGGTGAGTGTGTCCACGCCCATCGGGACATCT 360

Db 361 ACGAGCAGAGAAAGACGAGAGCGCTTCTCTATATAGTCTACGCCCTCCAGGAAACCT 420

Db
421 TCGGCTTCGAGCCAGCAGTAGGGGGCTGGCCCTGGAGTTCGGGGGGCCCCGGTACGC 480

db 481 CTTGCCGAGAGCTCTGTTCTTGAATCGAGCTGCTTACCGTGGTGGCTGGCGGCG 540

615 GCATGTCCCCCCTAGTCAGAGGCA 640

RESULT 6

DEFINITION Mus musculus RIKEN cDNA 4922501H04 gene, mRNA (cDNA clone MGC:6325 IMAGE:3256801), complete cds.

KEYWORDS
MUSCULUS (HOUSE MOUSE)
MGC.
DOI:10.1002/14001

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Sciurognathi; Muridae; Murinae; Mus.

Mausner, R. U., Collins, F. S., Wagner, L., Shemen, C. M., Schuler, G. D., Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bat, N. K.,

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 366)
 AUTHORS Kaindl, N., Chen, X., Rolfs, A., Halleck, A., Hines, L., Eisenstein, S., Koundinya, M., Raphael, J., Moreira, D., Kelley, T., Laber, J., Lin, Y., Phelan, M., and Farmer, A.
 TITLE Direct Submission
 JOURNAL Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow Circle, Palo Alto, CA 94303, USA
 COMMENT This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the SalI and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame. Clone distribution: <http://bioinfo.clontech.com/orfclones>.

FEATURES
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 /db_xref="taxon:9606"
 /clone="GH00946X1.0"
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 /lab_host="DH5alpha T1 resistant"
 /note="Vector: pDNR-Dual"
 1..366
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 BASE COUNT 84 a 116 c 101 g 65 t
 ORIGIN

Query Match 56.9%; Score 364; DB 9; Length 366;
 Best Local Similarity 100.0%; Pred. No. 1,9e-51;
 Matches 364; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

140 ATGCCCTCAGACCGCGCTTTTCAGCAGCGGCGAGCTTGGCCGAGCGCTGAAGAGGTA 199
 1 ATGCCCTCAGACCGCGCTTTTCAGCAGCGGCGAGCTTGGCCGAGCGCTGAAGAGGTA 60-
 200 CAGCAGATCCGCGACGACGACCCGACCAATCCCGGATCATCGAGCGCTACAAAGGT 259
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 260 GAGAAGCAGCTGCCCGCTCTGGACAGACCAAGTTTGGTCCCGGACCATGTCAACATG 319
 121 GAGAAGCAGCTGCCCGCTCTGGACAGACCAAGTTTGGTCCCGGACCATGTCAACATG 180
 320 AGCAGTTGGTCAAGATCATCCGCGCGCTGACGCTGAAGCAACCCAGCAGCGCTTCTTC 379
 181 AGCAGTTGGTCAAGATCATCCGCGCGCTGACGCTGAAGCAACCCAGCAGCGCTTCTTC 240
 380 CTGCTGGTGAACCGACGACGATGAGTGTCTCCACGCCCATTCGGGAGCATATACGAG 439
 241 CTGCTGGTGAACCGACGACGATGAGTGTCTCCACGCCCATTCGGGAGCATATACGAG 300
 440 CAGGAGAAGACGAGCAGCGCTTCTATATGCTACGCGCTCCAGGAACCTTCGGC 499
 301 CAGGAGAAGACGAGCAGCGCTTCTATATGCTACGCGCTCCAGGAACCTTCGGC 360
 500 TTCT 503
 361 TTCT 364

RESULT 8
 AX740487 1029 bp DNA Linear PAT 10-MAY-2003
 LOCUS Sequence 76 from Patent WO02020756.
 DEFINITION AX740487
 ACCESSION AX740487.1 GI:30523651
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 Stuart, J., Lincoln, S.E., Altus, C.M., Dufour, G., Chalup, M., Hillman, J.L., Jones, A.L., Yu, J.Y., Wright, R.J., Gietzen, D., Liu, T., Yap, P., Dahl, C.R., Momiyama, M.G., Bradley, D., Rohatyi, S., Harris, B., Roseberry, Ann, M., Gerstin, E.H., Peralta, C.H., David, M.H., Panzer, Scott, R., Flores, V., Daffo, A., Marwaha, R., Chen, A.J., Chang, S.C., Au, A.P., and Iman, R.R.
 Secretory molecules
 Patent: WO 02020756-A 76 14-MAR-2002;
 Incyte Genomics, Inc. (US)

TITLE
 JOURNAL
 Incyte Genomics, Inc. (US)
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 /note="Incyte ID No: LG:247776.14:2000SEP08"
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Query Match 46.5%; Score 297.8; DB 6; Length 1029;
 Best Local Similarity 99.3%; Pred. No. 2e-40;
 Matches 299; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

340 CCGCGCGCGCGCTGAGCTGAACCCAGCAGCGCTTCTCTCGTGTGACCCAGACAG 399
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 400 CATGCTAGTGTGTCAACGCCCATTCGCGAGCATCTACAGCAGAGAGAAGAGAGG 459
 614 CATGCTAGTGTGTGTCAACGCCCATTCGCGAGCATCTACAGCAGAGAGAAGAGAGG 673
 460 CTTCCTCTATATGTGTCTACGCTCCCAAGAACTTGGCTTGTGAGCCAGCAGTAGGG 519
 674 CTTCCTCTATATGTGTCTACGCTCCCAAGAACTTGGCTTGTGAGCCAGCAGTAGGG 733
 520 GGCTCGGCGCTGAGTGGGGGGGCGCGGTGAGCGCTTGGCCAGAGAGCTTGGTCT 579
 734 GGCTCGGCGCTGAGTGGGGGGGCGCGGTGAGCGCTTGGCCAGAGAGCTTGGTCT 793
 580 GAACCTGAGCTGCTCTACCGCTGTGTGGCTGGGACAGCATGTGCCCTTACTAGAGAGG 639
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 640 A 640
 854 A 854

RESULT 9
 HSA346K17 157975 bp DNA Linear PRI 19-OCT-2000
 LOCUS Human DNA sequence from clone Rpl1-346K17 on chromosome 20 Contains
 DEFINITION a novel gene encoding a protein similar to the cell division control protein 91 (CDC91) from yeast, a novel gene encoding two isoforms similar to MAP1ALC3 (microtubule-associated proteins 1A/1B lightchain 3) from Rat, 3 Cpg islands, ESTs, STS and GSSs, complete sequence.
 ACCESSION AL118520
 VERSION AL118520.26 GI:9801544
 KEYWORDS HTG: CDC91; Cpg island; microtubule-associated proteins.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominiidae: Homo.
1 (bases 1 to 157975)

REFERENCE
AUTHORS
TITLE
JOURNAL
Seftra,H.
Direct Submission
Submitted (19-Oct-2000) Sanger Centre, Hinxton, Cambridgeshire,
CH10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
Requests: clonerequest@sanger.ac.uk
On Aug 16, 2000 this sequence version replaced gi:5717213.

COMMENT
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL; SW: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr20

RP11-346K17 is from the library RPC1-11.2 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/vectors:pbac3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-346K17. It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true left end of clone RP11-346K17 is at 1 in this sequence. The true left end of clone RP5-1181N3 is at 157876 in this sequence. The true right end of clone RP5-914B9 is at 92396 in this sequence.

FEATURES

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19. 630
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86. 507
/note="match: GSS: Em:A0093367"
2783. 2959
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2964. 16247
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3543. 3896
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repeat_region
CDS

5554. 5943
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6639. 7044
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7334. 7542
/note="LIME2 repeat: matches 5825. 6044 of consensus"

7839. 7946
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repeat_region

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repeat_region

CDS

11729. 11890
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/evidence=not_experimental
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15345. 15412
/note="34 copies 2 mer cc 66% conserved"
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polyA-site

polyA-signal

CDS

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133031..133160))
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Em:AA317421 Em:AA157236 Em:AN354502
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PFAEMFENHSLEFVCFQJNVFFITPLIKLKEHIFPMFOIAVAITAFKSPYVGD
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Best Local Similarity 99.0%; Pred. No. 1.7e-40;
Matches 298; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

340 CCGGCGCGCGCTGACGTGAACCCACGACGAGCCCTTCTGCTGTGAACACGACAG 399
15808 CAGGCGCGCGCTGACGTGAACCCACGACGAGCCCTTCTGCTGTGAACACGACAG 15867
400 CATGCTGAGTGTGTCCAGCCCATCGGACATCTACGACGAGAGAAAGAGAGAGCG 459
15868 CATGCTGAGTGTGTCCAGCCCATCGGACATCTACGACGAGAGAGAAAGAGAGCG 15927
460 CTTCCTCTATATGCTCTACGCGCTCCAGAAACCTTGGCTTCTGAGCAGACAGAGG 519
15928 CTTCCTCTATATGCTCTACGCGCTCCAGAAACCTTGGCTTCTGAGCAGACAGAGG 15987
520 GGTCTGCGCGCTGGAGTCTGGGGGGCCCGGTCAGGCGCTCCAGAGAGCTTCTGGTCT 579
15988 GGTCTGCGCGCTGGAGTCTGGGGGGCCCGGTCAGGCGCTCCAGAGAGCTTCTGGTCT 16047
580 GAATGAGCTGCTCTACCGTGTGGGCTGGGAGGCAWGTGCCCCCTAGTCAAGAGGC 639
16048 GAATGAGCTGCTCTACCGTGTGGGCTGGGAGGCAWGTGCCCCCTAGTCAAGAGGC 16107
640 A 640
16108 A 16108

RESULT 10

AF255953

LOCUS AF255953 984 bp mRNA linear ROD 02-MAR-2002
DEFINITION Mus musculus MAP1A/1B light chain 3 subunit mRNA, complete cds.
ACCESSION AF255953
VERSION AF255953.1 GI:19070136
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 984)
AUTHORS Yu, L.
TITLE Direct Submission
JOURNAL Submitted (10-APR-2000) Institute of Genetics, Fudan University,
No. 220 Handan Road, Shanghai 200433, P.R. China
FEATURES
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1..984
/organism="Mus musculus"
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BASE COUNT 260 a 260 c 256 g 208 t
ORIGIN

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160 CAAGCAGCGCGAGCTTCGCGCGCGCTGTAGAGGAGTACGAGTCCGCGACACGA 219
96 CAAGCAGCGCGCGAGCTTTGACAAAGAGTGAAGATGCGGCTCATTCGCGAGACGA 155
220 CCCAGCAAAATCCGGGTGATCAGAGCGCTACAAAGGAGTGAAGAGAGCTGCGTCT 279
156 CCCACCAAAATCCAGATGATATAGAGGATACAAAGGAGGAGAGAGAGCTGCGTCT 215
280 GGACAAAGCAAAATTTTGTGTCGCGGACCATGTCAACATGAGCGAGTTGTCAGATCAT 339
216 GGACAAAGCAAAATTTTGTGTCGCGGACCATGTCAACATGAGCGAGTTGTCAGATCAT 275
340 CCGGCGCGCGCTGACGTGAACCCACGACGAGCCCTTCTGCTGTGAACACGACAG 399
276 CAGAGCGCGCTTGCAGCTCAATGCTAACCAAGCTTCTTCTCTGCTGTAATGGCACAG 335
400 CATGCTGAGTGTGTCCAGCCCATCGGACATCTACGACGAGAGAGAAAGAGAGAGCG 459
336 CATGCTGAGTGTGTCCAGCTCAATGCTAACCAAGCTTCTTCTCTGCTGTAATGGCACAG 395
460 CTTCCTCTATATGCTCTACGCGCTCCAGAAACCTTGGCTTCTGAGCAGACAGAGG 498
396 CTTCCTCTATATGCTCTACGCGCTCCAGAAACCTTGGCTTCTGAGCAGACAGAGG 434

RESULT 11

LOCUS AC116062 66877 bp DNA linear HTG 13-MAY-2003
DEFINITION Rattus norvegicus clone CH230-76N21, WORKING DRAFT SEQUENCE, 38
unordered pieces.
ACCESSION AC116062
VERSION AC116062.6 GI:30578911
KEYWORDS
SOURCE HTGS_PHASE1: HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus
 Mammalia: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
 Eumetazoa: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae:
Rattus.

REFERENCE
AUTHORS

1 (bases 1 to 66877)

Muzny,D.,Marle, Metzker,M.,Lee, Abramzon,S., Adams,C., Alder,J.,
 Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anquiano,D.,
 Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
 Baldwin,K., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
 Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
 Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
 Cardenas,V., Carter,K., Cavazos,I., Cesar,H., Center,A.,
 Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
 Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
 Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
 Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
 Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
 Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
 Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
 Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,I., Garza,M.,
 Gevorgis,E., Geer,K., Gill,R., Grady,M., Guerra,M., Guevara,W.,
 Gunaratne,P., Haaland,W., Hamill,C., Hamilton,C., Hamilton,K.,
 Harvey,Y., Havlik,P., Haves,A., Henderson,N., Hernandez,J.,
 Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hoques,M.,
 Hollins,B., Howells,S., Hulik,S., Hume,J., Idlebird,D., Jackson,A.,
 Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
 Kapachy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
 Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
 Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
 Lorensunwa,L., Louiseged,H., Lozada,R.J., Lu,X., Ma,J.,
 Maneswari,M., Mahindartine,M., Mahmoud,M., Malloy,K., Mangum,A.,
 Mangun,B., Mapua,P., Martin,K., Martin,M., Martinez,E.,
 Mashiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
 Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
 Morgan,M., Morris,K., Morris,S., Munitasa,M., Murphy,M., Natr,L.,
 Nakevicius,C., Neal,D., Newton,G., Olariunsaqoon,A., Pal,S., Parks,K.,
 Pasternak,S., Paul,H., Perez,A., Perez,L., Plankoch,C.,
 Plopper,F., Polidexter,A., Popovic,D., Primus,E., Pu,L.L.,
 Piazio,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
 Rellly,B., Rellly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
 Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
 Sanders,W., Savary,G., Scheier,S., Scott,G., Shatsman,S., Shen,H.,
 Shetty,J., Shvartsbeyn,A., Slisson,I., Sitter,C.D., Smajs,D.,
 Speed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
 Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
 Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmali,K.,
 Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
 Wang,O., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
 Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
 Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
 Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
 Niederhausen,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
 Weinstein,G., and Gibbs,R.A.

TITLE

Unpublished

2 (bases 1 to 66877)

Direct Submission

Submitted (24-MAR-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 66877)

Direct Submission

Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 66877)

Direct Submission

Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 66877)

Direct Submission

Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 66877)

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assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GNMW

Center clone name: CH230-76N21

----- Summary Statistics

Assembly program: Atlas 3.0?

Consensus quality: 5466 bases at least Q40

Consensus quality: 58172 bases at least Q30

Consensus quality: 60570 bases at least Q20

Estimated insert size: 39548; sum-of-contigs estimation

Quality coverage: 8x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length.
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 38 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1	1213:	contig of 1213 bp in length
1214	1313:	gap of unknown length
1314	2354:	contig of 1041 bp in length
2355	2454:	gap of unknown length
2455	3485:	contig of 1031 bp in length
3486	3585:	gap of unknown length
3586	4610:	contig of 1025 bp in length
4611	4710:	gap of unknown length
4711	5813:	contig of 1103 bp in length
5814	5913:	gap of unknown length
5914	6977:	contig of 1064 bp in length
6978	7077:	gap of unknown length
7078	8546:	contig of 1459 bp in length
8547	8646:	gap of unknown length
8647	9573:	contig of 1327 bp in length
9574	10073:	gap of unknown length
10074	11267:	contig of 1194 bp in length
11268	11367:	gap of unknown length
11368	12462:	contig of 1095 bp in length
12463	12562:	gap of unknown length
12563	13862:	contig of 1300 bp in length
13863	13962:	gap of unknown length
13963	15078:	contig of 1116 bp in length
15079	15178:	gap of unknown length
15179	16297:	contig of 1119 bp in length
16297	16397:	gap of unknown length
16398	18180:	contig of 1783 bp in length
18181	18280:	gap of unknown length
18281	19887:	contig of 1607 bp in length
19888	19987:	gap of unknown length
19989	21410:	contig of 1423 bp in length
21411	21510:	gap of unknown length
21511	23019:	contig of 1509 bp in length
23020	23119:	gap of unknown length
23120	24271:	contig of 1152 bp in length
24272	24371:	gap of unknown length
24372	25380:	contig of 1009 bp in length
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25481	26847:	contig of 1357 bp in length

FEATURES	location/Qualifiers
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	/clone="CH230-76N21"
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Db	31006	TCCGTCATATAGTGTATTATCCTTCGCGACGAGACTTCGG	31042
RESULT_12			
LOCUS	Ac103943/c		
DEFINITION	Ac103943	190843 bp	DNA linear HTG 21-AUG-2002
	Mus musculus clone RP23-460118,	WORKING DRAFT SEQUENCE,	6 ordered pieces.
ACCESSION	Ac103943		
VERSION	AC103943.3	GI:22381785	
KEYWORDS	HTG; HTGS; PHASE2; HTGS; DRAFT; HTGS_FULLTOP.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 190843)		
TITLE	Biren,B., Nusbaum,C. and Lander,E.		
JOURNAL	Mus musculus, clone RP23-460118		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 190843)		
	Biren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collimore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferrelle,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Glendire,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Larocque,K., Lamazeres,R., Landers,T., Lehoczyk,J., Levine,R., Liu,G., Maclean,C., MacDonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Menues,L., Mihova,T., Mlenka,Y., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schnupack,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tophan,K., Travers,M., Travis,N., Tigillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zemdek,L., Zimmer,A. and Zody,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
REFERENCE	3 (bases 1 to 190843)		
AUTHORS	Biren,B., Nusbaum,C., Lander,E., All,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collimore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferrelle,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Maclean,C., MacDonald,P., Major,J., Matthews,C., McCarthy,M., Meldrim,J., Menues,L., Mihova,T., Mlenka,Y., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schnupack,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Testfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zemdek,L., Zimmer,A. and Zody,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
COMMENT	On Aug 21, 2002 this sequence version replaced gi:19745075. All repeats were identified using RepeatMasker:		
	SmIt, A.F.A. & Green, P. (1996-1997)		

Dd		245	CAATGCTAACCAAGCCTTCTTCCTCCGTGGTAATGGGCACAGCATNGTAGTGTTGCCAC	304
OY		418	GCCATTGCGGACATCTACGACGACGAAGAAGACGAGACGGCTTCTATANGTCTA	477
Dd		305	ACCATTCTCTGAAAGTAGTAGAGAGAGAGAGATAMACGGCTCTGTACTGTCTTA	364
OY		478	CGCCTCCGAGAAACCTTCGG	498
Dd		365	TGCCTCCCAGAGACGTTCCG	385
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LOCUS		AX700303	861 bp	DNA linear PAT 03-APR-2003
DEFINITION		Sequence 72 from Patent EP1284297.		
ACCESSION		AX700303.1		
VERSION		AX700303.1 GI:29536157		
KEYWORDS		Rattus norvegicus (Norway rat)		
SOURCE		Rattus norvegicus		
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;		
REFERENCE		1 Brooksbank,R.A., Dixon,A.K., Lee,K. and Pimock,R.D. Identification and use of molecules implicated in pain Patent: EP 1284297-A 72 19-FEB-2003; WARNER-LAMBERT COMPANY (US) Location/Qualifiers		
AUTHORS		1..861	/organism="Rattus norvegicus"	
JOURNAL			/mol_type="genomic DNA"	
FEATURES			/db_xref="taxon:10116"	
source			/note="Light chain 3 subunit of microtubule-associated proteins 1A and 1B"	
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Best Local Similarity		76.6%;	Pred. No. 1.7e-30;	Matches 292;
Conservative		0;	Mismatches 89;	Indels 0;
Gaps		0;		
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Dd		5	CGAGCCAGAGACCCCCGCGCGCATGCGCTCCGAAGAACCCTTCAAAACAGCGCCGAGCTT	64
OY		178	CGCCGACCGCTGTAAAGAGGTACAGACAATCCGGACGACGCCACGCCAGAAAATCCGGT	237
Dd		65	CGAACAANAAGTGGABAATGTCCGGCTCATTCGGGAGACGACACCCACCAAGATCCAGT	124
OY		238	GATCATCGACGCGTACAAAGSGGTGAAGAACAGCTCCGCTCTGTGACAAGAACAAATTTTT	297
Dd		125	GATTATAGACGATACAAAGGTTGAGAAGACAGCTCCCGTCTGTGACAAGAACAAATTCCT	184
OY		298	GGTCCGAGACATGTCAACATGACCGAGTTGGTAAATCATTCGGCGCGCTTCGACGT	357
Dd		185	TGTACTGATCAGTACGTGATATGACCCAATCATCATAATATTGAAGGCGCCTGCAGCT	244
OY		358	GAACCCACACGAGCGCTTCTTCGCTGGTGGTGAACACGACAGCATGGTGAAGTGTCCAC	417
Dd		245	CAATGCTAACCAAGCCTTCTTCTCTCGTGGTGAATGGCACAGCATGGTGAAGTGTCCAC	304
OY		418	GCCCATGCGGACATCTACGACGACGAAGAAGACGAGACGGCTTCTATANGTCTA	477
Dd		305	ACCATTCTCTGAAAGTAGTAGAGAGAGAGATAMACGGCTCTGTACTGTCTTA	364
OY		478	CGCCTCCGAGAAACCTTCGG	498
Dd		365	TGCCTCCCAGAGACGTTCCG	385
RESULT_15				
RN005784				

LOCUS	RN005784	861 bp	mRNA	linear	ROD 11-AUG-1994
DEFINITION	Rattus norvegicus microtubule-associated proteins 1A and 1B light chain 3 subunit mRNA, complete cds.				
ACCESSION	U05784				
VERSION	U05784.1	GI:455108			
KEYWORDS					
SOURCE					
ORGANISM	Rattus norvegicus (Norway rat)				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
AUTHORS	Mann,S.S. and Hammarback,J.A.				
TITLE	Molecular characterization of light chain 3. A microtubule binding subunit of MAP1A and MAP1B				
JOURNAL	J. Biol. Chem. 269 (15), 11492-11497 (1994)				
MEDLINE	94209331				
PUBMED	7908909				
REFERENCE	2 (bases 1 to 861)				
AUTHORS	Hammarback,J.A.				
TITLE	Direct Submission				
JOURNAL	Submitted (28-JAN-1994) James A. Hammarback, Neurobiology and Anatomy, Bowman Gray School of Medicine, Medical Center Boulevard, Winston-Salem, NC 27157-1010, USA				
FEATURES	Location/Qualifiers				
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	/note="18 A residues"				
BASE COUNT	215 a	255 c	213 g	178 t	
ORIGIN					
Query Match	37.3%	Score 238.6;	DB 10;	Length 861;	
Best Local Similarity	76.6%;	Pred. NO. 1.7e-30;			
Matches 292;	Conservative 0;	Mismatches 89;	Indels 0;	Gaps 0;	
OY	118 CGCGCCAGCAGCCGGGCCCGCGCATGCCCTTCAGACCGGCCTTTCAAGCAGCGCGAGACTT	177			
Db					
	5 CGAGCCAGGAGACCOCGCCGCCGCGCATGCCGTCCGAAGAACCCTTCAACAGCGCCGAGACTT	64			
OY	178 CGCCGACCGCTGTAAAGAGAGTACAGCAGATCCGGAGCACGACACCACCCAGCAAATCCGGT	237			
Db					
	65 CGAACAAAGATGGAAAGATGTCGGGCTCAATCCGGAGACAGACCCCACAAGATGCCAGT	124			
OY	238 GATCATGACGACCGGTACAAAGGTGAGAAAGAGCTGCCGTCCTGGACAAGAACAAAGTTTTT	297			
Db					
	125 GATTATAGACGATPACAGGGTGAGAAAGAGCTGCCCCGTCCTGGACAAGACCAAGTTCCT	184			
OY	298 GGTCGCGGACCATGTCAACATGAGCGATGGTCAAGATCATCCGCGCGCCGCTGCAGCT	357			
Db					
	185 TGTAAGTAGATGACGTGAATATGAGCGAATCATCATAGATATTAATTAAGAAAGCGCCCTGCAGCT	244			
OY	358 GAACCCACGACGAGCCCTTCTTCCTGCTGTGAACACAGACAGCATGGTGAATGTGTCCAC	417			
Db					
	245 CATGCTTAACCAAGAGCTTCTTCCTCCGTTGGAAATGGGACACAGCATGGTGAATGTGTCCAC	304			
OY	418 GCCCATTCGGGACATCTACGACGAGGAAAAGACGAGAGCGCTTCTTATATATGTTCTA	477			
Db					

Db	405	ACCTATCTCTGAACTGTACGAGAGCGAGAGAGATGAAGCGGCTTCCTGTACATGTCTA	364
QY	478	CGCCTCCCGAGCAACTTCGG	498
Db	465	TGCTCCCGAGSAGAGTTGG	385

Search completed: August 15, 2003, 08:56:26
Job time : 2460 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 15, 2003, 04:50:54 ; Search time 258 seconds
(without alignments)
6696.280 Million cell updates/sec

Title: US-09-904-603-2
Perfect score: 640
Sequence: 1 CTCGCCGACGCGCCGCGCCGCGCCGCGCCGCGCGCA 640

Scoring table: IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	640	100.0	642	19	AAV43780
2	627.4	98.0	1000	24	ABQ54481
3	627	98.0	951	20	AAK20495
4	456.4	71.3	704	23	AAK37980
5	330.8	51.7	363	14	AAK61379
6	297.8	46.5	1029	24	AB199821
7	292	45.6	794	23	AAK37981
8	255.2	39.9	570	22	ABK61070

9	255.2	39.9	570	22	AAK6363
10	255.2	39.9	570	22	AAK35252
11	255.2	39.9	570	22	AAK14967
12	255.2	39.9	570	23	ABK4996
13	238.6	37.3	861	24	ABK61807
14	215.4	33.7	1910	24	AB199776
15	215	33.6	768	22	AA158815
16	215	33.6	791	22	AA195937
17	215	33.6	2250	21	AAK77815
18	215	33.6	2309	22	AA160602
19	215	33.6	3143	24	ABK64852
20	214.4	33.5	2199	24	ABK52817
21	212	33.1	515	22	AAK81833
22	192.4	30.1	537	24	ABK63294
23	174.2	27.2	870	21	AAK08590
24	163	25.5	163	22	AAK72009
25	163	25.5	163	22	AAK20434
26	163	25.5	163	22	AAK46575
27	163	25.5	163	22	AA152410
28	163	25.5	163	23	ABK46354
29	157.8	24.7	374	22	AAK5312
30	138.6	21.7	603	22	AAK52328
31	138.4	21.6	471	22	AAK61647
32	118.4	18.5	736	24	ABK4854
33	118.4	18.5	736	24	ABK4855
34	108.4	16.9	201	24	ABK52811
35	106.4	16.6	990	23	AAK70567
36	99.6	15.6	535	20	AAK20427
37	95.6	14.9	474	22	ABK42209
38	95.6	14.9	474	22	ABK52631
39	95.6	14.9	474	22	ABK22419
40	95.6	14.9	474	22	AAK00892
41	95.6	14.9	474	22	AAK26347
42	95.6	14.9	474	22	AA110980
43	95.6	14.9	474	22	AA132240
44	95.6	14.9	474	22	AA106501
45	95.6	14.9	474	23	ABK25938

ALIGNMENTS

RESULT 1	
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ID	AAV43780 standard; cDNA; 642 bp.
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AC	AAV43780;
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DT	20-NOV-1998 (first entry)
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DE	Human microtubule associated protein hM43 nucleotide sequence.
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KW	ss: human; microtubule-associated protein; hMAP; cell proliferation; cancer.
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XX	
OS	Homo sapiens.
XX	
PH	Key
FT	Location/Qualifiers
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PD	27-AUG-1996.
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PR	23-FEB-1998; 98W0-US03744.
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PR	24-FEB-1997; 97US-0805117.
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PA	(INCY-) INCYTE PHARM INC.
XX	
PI	Goli SK, Hillman JL;

Human brain expres
Human bone marrow
Probe #9653 used 1
Human liver single
Kat sequence clone
Human secretory po
Human polynucleoti
Human neuroblastom
Human cancer assoc
Human polynucleoti
Human tumor suppr
Genomic DNA enodi
Human Mpl's enodi
Kat sequence clone
Human cytoskeleton
Human foetal liver
Human brain expres
Human bone marrow
Probe #21096 used
Human liver single
Human polynucleoti
Human polynucleoti
Human fibroblastoma
Oligonucleotide to
Oligonucleotide to
cDNA encoding huma
DNA encoding novel
Human secreted pro
Human breast cell
Human foetal liver
Probe #885 for gen
Human brain expres
Human bone marrow
Probe #913 for gen
Probe #926 used to
Probe #892 used to
Human liver single

XX WPI: 1998-467560/40.
 DR P-PSDB: AAM69979.
 XX
 PT New isolated human micro:tubule-associated protein - used to develop
 PT products for use in the diagnosis, prevention and treatment of
 PT disorders associated with cell proliferation, particularly cancers
 XX
 PS Claim 5; Fig 1: 58pp; English.
 CC
 CC Human microtubule-associated protein (hMAP) expression is associated with
 CC disorders of cell proliferation, in particular, cancer. The hMAP and
 CC agonists can be used to stimulate cell proliferation. Tissues or
 CC organs generated by these methods may be introduced or transplanted into
 CC a subject for the purpose of treating a variety of diseases. Antagonists
 CC or inhibitors of hMAP can be used to treat or prevent disorders
 CC associated with cell proliferation, particularly cancers. The products
 CC can also be used for detection, diagnosis and drug screening.
 CC
 XX Sequence 642 BP; 121 A; 225 C; 199 G; 95 T; 2 other:

Query Match 100.0%; Score 640; DB 19; Length 642;
 Best Local Similarity 100.0%; Pred. No. 2,6e-129;

Matches 640: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTGGACGCGGACCGCCGCTGCTCAGCGGAGCCCGGAGCCCTTATGCGGAGCGC 60
 DB 3 CTCCTGGACGCGGACCGCCGCTGCTCAGCGGAGCCCGGAGCCCTTATGCGGAGCGC 62
 QY 61 GGAGCCCCGGAGCCCCCAACCGGACACATCCCGGCGCCCAAGCCCGGCGCTGGCG 120
 DB 63 GGAGCCCCGGAGCCCCCAACCGGACACATCCCGGCGCCCAAGCCCGGCGCTGGCG 122
 QY 121 GCCCAGCGGCGCGCGCGGATGCCCTCAGACCGCGCTTCAAGCAGCGCGGAGCTTGGC 180
 DB 123 GCCCAGCGGCGCGCGCGGATGCCCTCAGACCGCGCTTCAAGCAGCGCGGAGCTTGGC 182
 QY 181 CGACCGCTGTAAAGAGGTACAGCAGATCCGGACAGCACCACCAAAATCCCGGTAT 240
 DB 183 CGACCGCTGTAAAGAGGTACAGCAGATCCGGACAGCACCACCAAAATCCCGGTAT 242
 QY 241 CATCGAGCGCTACAAAGGTGAGAAAGCATCTGCCGCTCTGACAAAGACCAAGTTTGGT 300
 DB 243 CATCGAGCGCTACAAAGGTGAGAAAGCATCTGCCGCTCTGACAAAGACCAAGTTTGGT 302
 QY 301 CCGGACCATGTCAACATGAGCGAGTTGGTCAAGATCATCCGCGCCCGCTGCAAGTGA 360
 DB 303 CCGGACCATGTCAACATGAGCGAGTTGGTCAAGATCATCCGCGCCCGCTGCAAGTGA 362
 QY 361 CCCCACGAGGCGCTTCTTCTGCTGCTGTAACACAGCAGCATGGTGAAGTGTCCAGCC 420
 DB 363 CCCCACGAGGCGCTTCTTCTGCTGCTGTAACACAGCAGCATGGTGAAGTGTCCAGCC 422
 QY 421 CATCGGAGCATCTACGAGAGGAAAGAGAGAGGAGGCTTCTTATGAGTCTACAG 480
 DB 423 CATCGGAGCATCTACGAGAGGAAAGAGAGAGGAGGCTTCTTATGAGTCTACAG 482
 QY 481 CTCCAGGAAACCTTGGCTTCTGAGCCAGCAGTAGAGGGGCGCTGGAGTGGGG 540
 DB 483 CTCCAGGAAACCTTGGCTTCTGAGCCAGCAGTAGAGGGGCGCTGGAGTGGGG 542
 QY 541 GGGCCCGGTACGGCCCTGCGAGAGAGCTTGGTCTCTGAATGAGCTGCTTACCGT 600
 DB 543 GGGCCCGGTACGGCCCTGCGAGAGAGCTTGGTCTCTGAATGAGCTGCTTACCGT 602
 QY 601 GGTGGGCTGGGAGGAGCATGTGGCCCTAGTCAGAGGGCA 640
 DB 603 GGTGGGCTGGGAGGAGCATGTGGCCCTAGTCAGAGGGCA 642

RESULT 2
 AB054481
 ID AB054481 standard; cDNA: 1000 BP.

XX AB054481;
 AC 22-AUG-2002 (first entry)
 XX
 DT Human ovarian antigen HEATU31 cDNA, SEQ ID NO:361.
 XX
 DE Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200200677-A1.
 XX
 PD 03-JAN-2002.
 XX
 PF 07-JUN-2001; 2001WO-US18569.
 XX
 PA 07-JUN-2000; 2000US-209467P.
 XX
 PI (HUMA-) HUMAN GENOME SCI INC.
 XX
 PR Birse CE, Rosen CA;
 XX
 DR WPI: 2002-147878/19.
 XX
 P-PSDB: ABP41404.
 XX
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g.
 PT ovarian cancer), immune disorders, cardiovascular disorders and
 PT neurological diseases -
 XX
 PS Claim 1; SEQ ID NO 361; 2922pp; English.
 XX
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy; chromosome mapping; in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents cDNA encoding a human ovarian antigen of the
 CC invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

Sequence 1000 BP: 201 A; 337 C; 290 G; 171 T; 1 other:

Query Match 98.0%: Score 627.4; DB 24; Length 1000;

Best Local Similarity 99.7%: Pred. No. 1.5e-126; Mismatches 639; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```

QY 1 CTCCCGAGAGCCGAGCCGCTGCTCAGCCGAGAGCCCGAGCCCTTAGCGGAGGCG 60
   |||||||
Db 6 CTCCCGAGAGCCGAGCCGCTGCTCAGCCGAGAGCCCGAGCCCTTAGCGGAGGCG 65
QY 61 GGAG-CCCGGAGCCCGCCAAACCCAGACATCCCGCGCCAGAGCCCGGCTGCG 119
   |||||||
Db 66 GGAGCCCGCGAGCCCGCCAAACCCAGACATCCCGCGCCAGAGCCCGGCTGCG 125
QY 120 CGCCCGAGCCCGCGCGGCGATGCGCTCAGACCGGCTTTTCAAGCAGTGGGCGAGCTTGG 179
   |||||||
Db 126 CGCCCGAGCCCGCGCGGCGATGCGCTCAGACCGGCTTTTCAAGCAGTGGGCGAGCTTGG 185
QY 180 CCGAGCCGCTGTAAGAGAGTACAGCAGATCCGCGACAGCCCGCCAGAAATCCGCGTGA 239
   |||||||
Db 186 CCGAGCCGCTGTAAGAGAGTACAGCAGATCCGCGACAGCCCGCCAGAAATCCGCGTGA 245
QY 240 TCATCGAGCGCTACAGAGGTGAGAGCAGCTGCCCGCTCTGGACAGACCAAGTTTGG 299
   |||||||
Db 246 TCATCGAGCGCTACAGAGGTGAGAGCAGCTGCCCGCTCTGGACAGACCAAGTTTGG 305
QY 300 TCCCCGAGCATGTCAACATGAGCGAGTTGCTCAGATCATCCGCGCGCCCTCGAGCTGA 359
   |||||||
Db 306 TCCCCGAGCATGTCAACATGAGCGAGTTGCTCAGATCATCCGCGCGCCCTCGAGCTGA 365
QY 360 ACCCGCAGCAGAGCCCTTCTCTGCTGTGAGACAGCAGATGATGATGTTGTCACGC 419
   |||||||
Db 366 ACCCGCAGCAGAGCCCTTCTCTGCTGTGAGACAGCAGATGATGATGTTGTCACGC 425
QY 420 CCATCGCGGAGCATTCAGACAGAGAAAGACAGAGCGCTTCTCTATATGCTACAG 479
   |||||||
Db 426 CCATCGCGGAGCATTCAGACAGAGAAAGACAGAGCGCTTCTCTATATGCTACAG 485
QY 480 CCTCCGAGGAAGCCTTGGCTTGTGAGCAGCAGTAGGGGGGCTCGGCTGAGTGGG 539
   |||||||
Db 486 CCTCCGAGGAAGCCTTGGCTTGTGAGCAGCAGTAGGGGGGCTCGGCTGAGTGGG 545
QY 540 GGGCGCGCGGTGAGGCGCTTGGCCAGAGAGCTTGTGTTCTGAACTGAGCTGCTTACCG 599
   |||||||
Db 546 GGGCGCGCGGTGAGGCGCTTGGCCAGAGAGCTTGTGTTCTGAACTGAGCTGCTTACCG 605
QY 600 TGGTGGGCTGGGCGAGCATGTGCCCGCTAGTCAAGAGGCGCA 640
   |||||||
Db 606 TGGTGGGCTGGGCGAGCATGTGCCCGCTAGTCAAGAGGCGCA 646

```

Result 3
AAAX20495

ID AAX20495 standard; DNA: 951 BP.

AC AAX20495:

DT 04-MAY-1999 (first entry)

DE Human secreted protein gene.

DE Human; secreted protein; fusion protein; gene therapy; protein therapy;

KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;

KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;

KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;

KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;

KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;

KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;

KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm;

OS Homo sapiens.

XX W9906423-A1.

```

XX 11-FEB-1999.
PD 19-AUG-1997; 97US-0056740.
XX 30-JUL-1997; 97US-0054209.
XX 30-JUL-1997; 97US-0054211.
PF 29-JUL-1998; 98W0-US15949.
XX 19-AUG-1997; 97US-0054212.
PR 30-JUL-1997; 97US-0054213.
PR 30-JUL-1997; 97US-0054214.
PR 30-JUL-1997; 97US-0054215.
PR 30-JUL-1997; 97US-0054218.
PR 30-JUL-1997; 97US-0054234.
PR 30-JUL-1997; 97US-0054236.
PR 18-AUG-1997; 97US-0055968.
PR 18-AUG-1997; 97US-0055969.
PR 18-AUG-1997; 97US-0055972.
PR 18-AUG-1997; 97US-0056534.
PR 19-AUG-1997; 97US-0056543.
PR 19-AUG-1997; 97US-0056554.
PR 19-AUG-1997; 97US-0056561.
PR 19-AUG-1997; 97US-0056727.
PR 19-AUG-1997; 97US-0056729.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX Carter KC, Endress GA, Fan P, Feng P, Kyaw H, Lafleur MW;
PI Li Y, Moore PA, Kosen CA, Ruben SM, Shi Y, Wei Y;
PI Zeng Z;
XX WPI: 1995-153691/13.
XX P-PSDB: AAY00340.
XX
XX New isolated human genes and the secreted polypeptides they encode -
PI useful for diagnosis and treatment of e.g. cancers, neurological
PI disorders, immune diseases, inflammation or blood disorders
XX
XX PS Disclosure: Page 249; 312pp; English.
XX
XX This sequence represents a nucleic acid molecule which encodes a
CC secreted human protein. The gene number is given in the description line.
CC The gene can be used to generate fusion proteins by linking the gene
CC to a human immunoglobulin Fc portion (e.g. AAX20403) for increasing the
CC stability of the fused protein as compared to the human protein only.
CC The invention relates to 84 novel genes and their transcripts (nucleic
CC acid sequences: AAX20412-X20499; amino acid sequences AAY00258-Y00477)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 84
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAX20412 for described uses).
XX
XX Sequence 951 BP: 159 A; 332 C; 287 G; 170 T; 3 other:

```

Query Match 98.0%: Score 627; DB 20; Length 951;

Best Local Similarity 99.5%: Pred. No. 1.8e-126;

Matches 638; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

```

QY 1 CTCCCGCAGATGCGAGTGGCGTGTGAGTGGAGGCGGAGCGCTTAGTGGAGGTCG 60
   |||||||
Db 6 CTCCCGCAGATGCGAGTGGCGTGTGAGTGGAGGCGGAGCGCTTAGTGGAGGTCG 65
QY 61 GGAG-CCCGGAGCCCGCCAAACCCAGACATCCCGCGCCAGAGCCCGGCTGCG 119
   |||||||
Db 66 GGAGCCCGCGAGCCCGCCAAACCCAGACATCCCGCGCCAGAGCCCGGCTGCG 125
QY 120 CGCCCGAGTGGGCGCGCGGAGATGCGCTCAGACCGGCTTTTCAAGTAGGCGGCGAGCTTGG 179
   |||||||
Db 126 CGCCCGAGTGGGCGCGCGGAGATGCGCTCAGACCGGCTTTTCAAGTAGGCGGCGAGCTTGG 185

```

QY 180 CCGACGGCTGTAGAGGTACACAGATCCGCGACCCAGCACCAGCAAAATCCGGTGA 239
 DB 186 CCGACGGCTGTAGAGGTACACAGATCCGCGACCCAGCACCAGCAAAATCCGGTGA 245
 QY 240 TCATCAGGCGTACAGAGGTGAGAACAGTCCGCTCGTGGACAGACCAAGTTTGG 299
 DB 246 TCATCAGGCGTACAGAGGTGAGAACAGTCCGCTCGTGGACAGACCAAGTTTGG 305
 QY 300 TCCCGGACCATGTCAACATGAGCGAGTGGTCAATCATCCGCGCCGCTGACACTGA 359
 DB 306 TCCCGGACCATGTCAACATGAGCGAGTGGTCAATCATCCGCGCCGCTGACACTGA 365
 QY 360 ACCCCAGGAGGCGTCTCTCGTGGTGAACACAGACAGCATGATGTGTCCAGCG 419
 DB 366 ACCCCAGGAGGCGTCTCTCGTGGTGAACACAGACAGCATGATGTGTGTCCAGCG 425
 QY 420 CCATCGCGGACATCTACAGAGCAGAGAGAGAGGCGTCTCTATATGATGTAG 479
 DB 426 CCATCGCGGACATCTACAGAGCAGAGAGAGAGGCGTCTCTATATGATGTAG 485
 QY 480 CTTCCAGGAACTTCGCGCTTCTGTAGCCAGCATAGTGGGGGCTCGCCTGGAGTGGG 539
 DB 486 CTTCCAGGAACTTCGCGCTTCTGTAGCCAGCATAGTGGGGGCTCGCCTGGAGTGGG 545
 QY 540 GGGCCCCGGTCAAGGCGCTTCTGTAGCCAGCATAGTGGGGGCTCGCCTGGAGTGGG 599
 DB 546 GGGCCCCGGTCAAGGCGCTTCTGTAGCCAGCATAGTGGGGGCTCGCCTGGAGTGGG 605
 QY 600 TGGTGGGCTGGGAGGAGCATGTGCCCCCTAGTACAGAGGCA 640
 DB 606 TGGTGGGCTGGGAGGAGCATGTGCCCCCTAGTACAGAGGCA 646

RESULT 4
 AAS73980
 ID AAS73980 standard; cDNA: 704 BP.
 AC AAS73980;
 XX

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #9784.

KM Human: chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.

DR P-PSDB: ABG09793.

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity

PS Claim 1; SEQ ID No 9784; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences.

SQ Sequence 704 BP; 131 A; 263 C; 191 G; 119 T; 0 other;

Query Match 71.3%; Score 456.4; DB 23; Length 704;
 Best Local Similarity 98.8%; Pred. No. 1.3e-89;
 Matches 512; Conservative 0; Mismatches 1; Indels 5; Gaps 5;

QY 1 CTCGCCAGCCGCGCGCGCTGTCTACAGGCGGAGCGCCGCGGACCTTGAGCGCGAGGCC 60
 DB 15 CTCGCCAGCCGCGCGCGCGCTGTCTACAGGCGGAGCGCCGCGGACCTTGAGCGCGAGGCC 74
 QY 61 GGAG-CGCCGAGCCGCCAAGCCAGACATCCCGCGGCCAGAGGCCCGCGCTGG 119
 DB 75 GGAGCCCGCGGAGCCGCCAAGCCAGACATCCCGCGGCCAGAGGCCCGCGCTGG 134
 QY 120 GCGCCAGCGGGCGCGCGCGATGCTTACAGACCGCTTCAAGCAGCGCGGAGCTTGC 179
 DB 135 GCGCCAGCGGGCGCGCGCGATGCTTACAGACCGCTTCAAGCAGCGCGGAGCTTGC 194
 QY 180 CCGA-CCGCTGTAAAGAGGTACAGAGATCCG-CGACGACGACCCAGCAAAATCCCGGT 237
 DB 195 CCGACCGCGCTGTAAAGAGGTACAGAGATCCGCGACGACGCCAGCAAAATTCGGGT 254
 QY 238 -GATCATGAGCGCTTCAAGAGGTGAGAGACAGCTCCGCTGTGACAAGACCAAGTTT 296
 DB 255 GATCATGAGCGCTTCAAGAGGTGAGAGACAGCTCCGCTGTGACAAGACCAAGTTT 314
 QY 297 TGGTCCGCGACCATGTCAACATGAGCGAGTGGTCAATATCTCCGGCGCGCTGACAGC 356
 DB 315 TGGTCCGCGACCATGTCAACATGAGCGAGTGGTCAATATCTCCGGCGCGCTGACAGC 374
 QY 357 TGAACCCGACGAGCGCTTCTCTGCTGTGTAACACAGCAGCATGTGTGAGTGTG-TCC 415
 DB 375 TGAACCCGACGAGCGCTTCTCTGCTGTGTAACACAGCAGCATGTGTGAGTGTG-TCC 434
 QY 416 AGGCCCATGCGGAGCATGTACAGAGGAGAAAGCGAGAGCGCTTCTATATGTGTC 475
 DB 435 AGGCCCATGCGGAGCATGTACAGAGGAGAAAGCGAGAGCGCTTCTATATGTGTC 494
 QY 476 TAGGCGTCCAGGAACCTTGGGCTTGTGAGCCAGAGCAG 513
 DB 495 TAGGCGTCCAGGAACCTTGGGCTTGTGAGCCAGAGCAG 532

RESULT 5
 AAO61379
 ID AAO61379 standard; DNA: 363 BP.
 XX AAO61379;
 AC

DT 25-MAR-2003 (updated)
 DT 16-MAR-1994 (first entry)

DE Human brain Expressed Sequence Tag EST01371.
 XX
 XX Gene transcription product: genetic markers; tagging: in vivo;
 KW transcription; mapping; locations; chromosomes; chromosomal; ss.
 XX
 OS Homo sapiens.
 XX
 XX W09316178-A2.
 XX
 XX 19-AUG-1993.
 PD
 XX 12-FEB-1993: 93WO-US01294.
 PF
 XX 12-FEB-1992: 92US-0837195.
 FR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICE.
 PA
 XX Adams MD, Moreno RF, Ventler CJ;
 P1
 XX WPI: 1993-272882/34.
 DR
 XX
 XX Enriched oligonucleotides and corresp. sequences - used as
 PT markers for human genes transcribed in-vivo, facilitate tagging
 PT of most human genes
 PS
 XX Example 4; Page 482; 500pp; English.
 PS
 XX The Expressed Sequence Tag was isolated from a human brain cDNA
 CC library as part of a large set of ESTs which can be used as markers
 CC for human genes transcribed in vivo. They can be used to facilitate
 CC tagging of most human genes, for mapping locations of expressed genes
 CC on chromosomes, for individual or forensic identification, for mapping
 CC locations of disease-associated genes, for identification of tissue
 CC type, and for prepn. of antisense sequences, probes and constructs.
 CC EST01371 has a "excellent" coding probability as evaluated using the
 CC coding-region prediction program CRM. See also A059041-061440.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX Sequence 363 BP; 84 A; 108 C; 99 G; 66 T; 6 other:
 SO
 Query Match 51.7%; Score 330.8; DB 14; Length 363;
 Best Local Similarity 97.3%; Pred. No. 1.8e-62;
 Matches 354; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

153 GGCCTTTACAGCAGCGCGGAGCTTCGCCGACCGCTGTGAAGAGGTACACGACATCCCG 212
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 1 GGCCTTTCAAGNAGCGGCGGA-NTTCGCCGACCGCTGTAGAGGTACAGCAGATCCCG 59
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 213 ACCAGACCCCGACAAATCCGGTATCATGACCGCTACAGAGGTGAGAAAGAGTGC 272
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 60 ACCAGACCCCGACAAATCCCGGATCATGACCGCTACAGAGGTGAGAAAGAGTGC 119
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 273 CCGTCTGGACAGACCAAGTCTTGTCTCCGAGACCATGTCAACATGAGCGAGTTGCTA 332
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 120 CCGTCTGGACAGACCAAGTCTTGTCTCCGAGACCATGTCAACATGAGCGAGTTGCTA 179
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 333 AGATCATCGGGCGCGCTGAGGTGAGACCCGACGCGCTTCTTCTGCTGTGAGCC 392
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 180 AGATCATCGGGCGCGCTGAGGTGAGACCCGACGCGCTTCTTCTGCTGTGAGCC 239
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 393 AGCAGCAGTGTGTCTGCAAGCCCATGCGGACATCTACAGAGAGAGAAAGAGC 452
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 240 AGCAGCAGTGTGTGTCTGCAAGCCCATGCGGACATCTACAGAGAGAGAAAGAGC 299
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 453 AGAAGGCTTCTCTATATGTGTCTAGCGCTCCAGAAACCTTCGGC-TTCTGAGCCAGC 511
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 300 AGAAGGCTTCTCTATATGTGTCTAGCGCTCCAGAAACCTTCGGCTTCTGAGNCAGC 359
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 512 AGTA 515
 |||||
 360 AGTA 363

RESULT 6
 ABL99821
 ID ABL99821 standard; cDNA; 1029 BP.
 XX
 XX ABL99821;
 AC
 XX
 XX 03-OCT-2002 (first entry)
 DT
 XX
 XX Human secretory polynucleotide (sptm) 76.
 DE
 XX
 XX Human; ss; gene; secretory protein; secretory polynucleotides; SPTM;
 KW SPTM-related disease; somatic gene therapy; demiline gene therapy;
 KW severe combined immunodeficiency; intracellular parasite protection;
 KW fungal parasite; protozoan parasite; cell proliferative disorder; cancer;
 KW immune disorder; AIDS; neurological disorder; Parkinson's disease;
 KW motor neuron disorder; demyelinating disease; multiple sclerosis;
 KW meningitis; abscess; prion diseases; cerebral palsy;
 KW neuroskeletal disorder; peripheral nervous system disorder;
 KW dermatomyositis; polymyositis; myopathy; myasthenia gravis;
 KW mental disorder; Loureite's syndrome.
 XX
 OS Homo sapiens.
 XX
 XX W0200220756-A2.
 PN
 XX
 XX 14-MAR-2002.
 PD
 XX
 XX 30-AUG-2001: 2001WO-US27297.
 PF
 XX
 XX 05-SEP-2000: 2000US-229747P.
 PR
 XX 05-SEP-2000: 2000US-229748P.
 PR
 XX 05-SEP-2000: 2000US-229749P.
 PR
 XX 05-SEP-2000: 2000US-229750P.
 PR
 XX 05-SEP-2000: 2000US-229751P.
 PR
 XX 05-SEP-2000: 2000US-230016P.
 PR
 XX 05-SEP-2000: 2000US-230583P.
 PR
 XX 05-SEP-2000: 2000US-230585P.
 PR
 XX 05-SEP-2000: 2000US-230596P.
 PR
 XX 05-SEP-2000: 2000US-230597P.
 PR
 XX 05-SEP-2000: 2000US-230599P.
 PR
 XX 05-SEP-2000: 2000US-230610P.
 PR
 XX 05-SEP-2000: 2000US-230644P.
 PR
 XX 05-SEP-2000: 2000US-230865P.
 PR
 XX 05-SEP-2000: 2000US-230988P.
 PR
 XX 05-SEP-2000: 2000US-230989P.
 PR
 XX 05-SEP-2000: 2000US-230990P.
 PR
 XX 05-SEP-2000: 2000US-230996P.
 PR
 XX 05-SEP-2000: 2000US-230897P.
 PR
 XX 05-SEP-2000: 2000US-230951P.
 PR
 XX 05-SEP-2000: 2000US-231163P.
 PR
 XX 05-SEP-2000: 2000US-231832P.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 PA
 XX
 XX Stuart J, Lincoln SE, Altus CM, Dutoir GE, Chalup MS, Hillman JL;
 PI Jones AL, Yu JY, Wright RJ, Gietzen U, Liu TF, Yap PF, Dahl CK;
 PI Momiyama MC, Bradley DL, Kohatgi SD, Harris B, Roseberry AM;
 PI Gerstin EH, Petalita CH, David MB, Panzer SR, Flores V, Datto A;
 PI Marwaha R, Chen AJ, Chang SC, Au AP, Imman RR;
 PI WPI: 2002-315658/35.
 DR P-PSDB; ABB97824.
 XX
 XX Polynucleotide sequences encoding human secretory proteins useful for
 PT gene therapy of e.g. genetic deficiency disorders, cancers, and
 PT diseases caused by intracellular parasites -

Db 421 GCAGGCGATGTGCCCCC 438

RESULT 8

ABAb1070 ID ABAb1070 standard; DNA: 570 BP.

XX AC ABAb1070;

XX DT 01-FEB-2002 (first entry)

XX XX Human foetal liver single exon nucleic acid probe #9375.

XX KW Human: foetal liver; gene expression; single exon nucleic acid probe; ss.

XX OS Homo sapiens.

XX PN W0200157277-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001W0-US00669.

XX PR 04-FEB-2000; 2000US-0180312.

XX PR 26-MAY-2000; 2000US-0207456.

XX PR 30-JUN-2000; 2000US-0608408.

XX PR 03-AUG-2000; 2000US-0632366.

XX PR 21-SEP-2000; 2000US-0234687.

XX PR 27-SEP-2000; 2000US-0236359.

XX PR 04-OCT-2000; 2000GB-0024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DK;

XX DT WPI: 2001-483447/52.

XX PT Human genome-derived single exon nucleic acid probes useful for

XX PI analyzing gene expression in human fetal liver -

XX PS Claim 1: SEQ ID NO 9375; 639pp + sequence listing; English.

XX CC The invention relates to a single exon nucleic acid probe for

XX CC measuring human gene expression in a sample derived from human foetal

XX CC liver. The single exon nucleic acid probes may be used for predicting,

XX CC measuring and displaying gene expression in samples derived from human

XX CC foetal liver. The present sequence is a single exon nucleic acid

XX CC probe of the invention.

XX CC Note: The sequence data for this patent did not form part of the

XX CC printed specification, but was obtained in electronic format directly

XX CC from WIPO at ftp.wipo.int/pub/published_pcr_sequences.

XX SQ Sequence 570 BP: 97 A; 158 C; 213 G; 102 T; 0 other;

Query Match 39.9%; Score 255.2; DB 22; Length 570;
Best Local Similarity 98.8%; Pred. No. 4.3e-46;
Matches 257; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 340 CGCGGCGCGCTGAGCTGAACCCGACGAGGCTCTTCTGCTGTGAACGACAG 399

Db 311 CAGGCGCGCGCTGAGCTGAACCCGACGAGGCTCTTCTGCTGTGAACGACAG 370

QY 400 CATGTGAGTGTGTCCAGCGCCATCGGGGACATCTACAGAGAGGAAGACGAGAGG 459

Db 371 CATGTGAGTGTGTCCAGCGCCATCGGGGACATCTACAGAGAGGAAGACGAGAGG 430

QY 460 CTTCCTATATAGTCTACGGCTCCAGGAACCTTGGCTTGTAGCCACAGTAGGG 519

Db 431 CTTCCTATATAGTCTACGGCTCCAGGAACCTTGGCTTGTAGCCACAGTAGGG 490

QY 520 GCGTGGGCTGTGGAGTGGGGGGCCCGGCTGAGGCCCTGCCAGAGAGCTTCTGTTCT 579

Db 491 GCGTGGGCTGTGGAGTGGGGGGCCCGGCTGAGGCCCTGCCAGAGAGCTTCTGTTCT 550

QY 580 GAAGTGAAGTGTGTACAG 599

Db 551 GAAGTGAAGTGTGTACAG 570

RESULT 9

AAK09363 ID AAK09363 standard; DNA: 570 BP.

XX AC AAK09363;

XX DT 05-NOV-2001 (first entry)

XX DE Human brain expressed single exon probe SEQ ID NO: 9354.

XX XX Human: brain expressed exon; gene expression analysis; probe;

XX KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;

XX KW epilepsy; cancer; ss.

XX OS Homo sapiens.

XX PN W0200157275-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001W0-US00667.

XX PR 04-FEB-2000; 2000US-0180312.

XX PR 26-MAY-2000; 2000US-0207456.

XX PR 30-JUN-2000; 2000US-0608408.

XX PR 03-AUG-2000; 2000US-0632366.

XX PR 21-SEP-2000; 2000US-0234687.

XX PR 27-SEP-2000; 2000US-0236359.

XX PR 04-OCT-2000; 2000GB-0024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DK;

XX DT WPI: 2001-483446/52.

XX PT Single exon nucleic acid probes for analyzing gene expression in human

XX PI brains -

XX PS Example 4: SEQ ID NO: 9354; 650pp + Sequence listing; English.

XX CC The present invention provides a number of single exon nucleic acid

XX CC probes which are derived from genomic sequences expressed in the human

XX CC brain. They can be used to measure gene expression in brain cell samples,

XX CC which may enable the diagnosis and improved treatment of nervous system

XX CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

XX CC epilepsy and cancers. The present sequence is one of the probes of the

XX CC invention.

XX SQ Sequence 570 BP: 97 A; 158 C; 213 G; 102 T; 0 other;

Query Match 39.9%; Score 255.2; DB 22; Length 570;
Best Local Similarity 98.8%; Pred. No. 4.3e-46;
Matches 257; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 340 CGCGGCGCGCTGAGCTGAACCCGACGAGGCTCTTCTGCTGTGAACGACAG 399

Db 311 CAGGCGCGCGCTGAGCTGAACCCGACGAGGCTCTTCTGCTGTGAACGACAG 370

QY 400 CATGTGAGTGTGTCCAGCGCCATCGGGGACATCTACAGAGAGGAAGACGAGAGG 459

Db 371 CATGTGAGTGTGTCCAGCGCCATCGGGGACATCTACAGAGAGGAAGACGAGAGG 430

QY 460 CTTCCTATATAGTCTACGGCTCCAGGAACCTTGGCTTGTAGCCACAGTAGGG 519

Db 431 CTTCCTATATAGTCTACGGCTCCAGGAACCTTGGCTTGTAGCCACAGTAGGG 490

OY 520 GGCCTGAGCTGGAGATCGGGGCCCCGGTCAGGCGCTTCCAGAGACTTCTGTTCT 579
 DB 491 GGCCTGAGCTGGAGATCGGGGCCCCGGTCAGGCGCTTCCAGAGACTTCTGTTCT 550
 OY 580 GAAGTGAAGCTGCTCTTACC 599
 DB 551 GAAGTGAAGCTGCTCTTACC 570

RESULT 10

AAK35252 ID AAK35252 standard; DNA: 570 BP.

AAK35252; AC

06-NOV-2001 (first entry) DT

Human bone marrow expressed single exon probe SEQ ID NO: 9809. DE

Human: bone marrow expressed exon; gene expression analysis; probe; KW

microarray; cancer; leukemia; lymphoma; myeloma; ss. KM

Homo sapiens. OS

WO200157276-A2. PN

09-AUG-2001. PD

30-JAN-2001; 2001WO-US00668. PF

04-FEB-2000; 2000US-0180312. PR

26-MAY-2000; 2000US-0207456. PR

30-JUN-2000; 2000US-0608408. PR

03-AUG-2000; 2000US-0632366. PR

21-SEP-2000; 2000US-0234687. PR

27-SEP-2000; 2000US-0236359. PR

04-OCT-2000; 2000GB-0024263. PR

(MOLE-) MOLECULAR DYNAMICS INC. PA

Penn SG, Hanzel DK, Chen W, Rank DR; PI

WPI; 2001-488900/53. DR

Human genome-derived single exon nucleic acid probes useful for PT

analyzing gene expression in human bone marrow. PS

Example 4; SEQ ID NO: 9809; 658bp + sequence listing; English. PS

The present invention provides a number of single exon nucleic acid CC

probes which are derived from genomic sequences expressed in the human CC

bone marrow. They can be used to measure gene expression in bone marrow CC

samples, which may enable the improved diagnosis and treatment of cancers CC

such as lymphoma, leukemia and myeloma. The present sequence is one of CC

the probes of the invention. XX

Sequence 570 BP; 97 A; 158 C; 213 G; 102 T; 0 other; SQ

Query Match 39.9%; Score 255.2; DB 22; Length 570; Best Local Similarity 98.8%; Pred. No. 4.3e-46; Matches 257; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 340 CCGGCGCGCTGAGCTGAACCCAGCAGGCGCTTCTCTGCTGAGACGACGACAG 399

DB 311 CAGGCGCGCTGAGCTGAACCCAGCAGGCGCTTCTCTGCTGAGACGACGACAG 370

OY 400 CATGCTAGTGTGTCCACGCCATCGCGGACATCTACGACGAGAGAAAGACGAGACG 459

DB 371 CATGCTAGTGTGTCCACGCCATCGCGGACATCTACGACGAGAGAAAGACGAGACG 430

OY 460 CTTCTCTATATGCTTACGCGCTCCAGAGAAACCTTGGCTTGTAGCCACAGTAGGG 519

DB 431 CTTCTCTATATGCTTACGCGCTCCAGAGAAACCTTGGCTTGTAGCCACGATAGGG 490
 OY 520 GGCCTGAGCTGGAGATCGGGGCCCCGGTCAGGCGCTTCCAGAGACTTCTGTTCT 579
 DB 491 GGCCTGAGCTGGAGATCGGGGCCCCGGTCAGGCGCTTCCAGAGACTTCTGTTCT 550
 OY 580 GAAGTGAAGCTGCTCTTACC 599
 DB 551 GAAGTGAAGCTGCTCTTACC 570

RESULT 11

AAI40967 ID AAI40967 standard; DNA: 570 BP.

AAI40967; AC

17-OCT-2001 (first entry) DT

Probe #9653 used to measure gene expression in human placenta sample. DE

Probe; microarray; human; placenta; antenatal diagnosis; KW

genetic disorder; ss. KM

Homo sapiens. OS

WO200157272-A2. PN

09-AUG-2001. PD

30-JAN-2001; 2001WO-US00663. PF

04-FEB-2000; 2000US-0180312. PR

26-MAY-2000; 2000US-0207456. PR

30-JUN-2000; 2000US-0608408. PR

03-AUG-2000; 2000US-0632366. PR

21-SEP-2000; 2000US-0234687. PR

27-SEP-2000; 2000US-0236359. PR

04-OCT-2000; 2000GB-0024263. PR

(MOLE-) MOLECULAR DYNAMICS INC. PA

Penn SG, Hanzel DK, Chen W, Rank DR; PI

WPI; 2001-48897/53. DR

Human genome-derived single exon nucleic acid probes useful for PT

analyzing gene expression in human placenta. PS

Claim 25; SEQ ID No 9653; 654bp; English. PS

The present invention relates to single exon nucleic acid probes (SENPs). CC

The present sequence is one such probe. The probes are useful for CC

producing a microarray for predicting, measuring and displaying gene CC

expression in samples derived from human placenta. The probes are useful CC

for antenatal diagnosis of human genetic disorders. XX

Sequence 570 BP; 97 A; 158 C; 213 G; 102 T; 0 other; SQ

Query Match 39.9%; Score 255.2; DB 22; Length 570; Best Local Similarity 98.8%; Pred. No. 4.3e-46; Matches 257; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 340 CCGGCGCGCTGAGCTGAACCCAGCAGGCGCTTCTCTGCTGAGACGACGACAG 399

DB 311 CAGGCGCGCTGAGCTGAACCCAGCAGGCGCTTCTCTGCTGAGACGACGACAG 370

OY 400 CATGCTAGTGTGTCCACGCCATCGCGGACATCTACGACGAGAGAAAGACGAGACG 459

DB 371 CATGCTAGTGTGTCCACGCCATCGCGGACATCTACGACGAGAGAAAGACGAGACG 430

OY 460 CTTCTCTATATGCTTACGCGCTCCAGAGAAACCTTGGCTTGTAGCCACAGTAGGG 519

Db 431 CTCTCTATATGCTTACGGCTCCAGAAACCTTCGGCTTCTGAGCCAGACTAGGG 490
 QY 520 GGCTCGGCTGGAGTGGGGGGCCCGGTGAGGCTTCCAGAGACTTCTGTTCT 579
 Db 491 GGCTCGGCTGGAGTGGGGGGCCCGGTGAGGCTTCCAGAGACTTCTGTTCT 550
 QY 580 GAAGTGAAGTGGCTTCTACCG 599
 Db 551 GAAGTGAAGTGGCTTCTACCG 570

RESULT 12

ABK34996
 ID ABS34996 standard; DNA: 570 BP.
 AC ABS34996:
 XX 25-FEB-2003 (first entry)
 XX Human liver single exon probe, SEQ ID No 9986.
 DE Human liver single exon probe, SEQ ID No 9986.
 XX
 KW Human: single exon nucleic acid probe; liver; cirrhosis;
 KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
 KW coronary heart disease; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200157273-A2.
 XX 05-AUG-2001.
 XX 30-JAN-2001: 2001WO-0500664.
 XX
 PR 04-FEB-2000: 2000US-0180312.
 PR 26-MAY-2000: 2000US-0207456.
 PR 30-JUN-2000: 2000US-0608408.
 PR 03-AUG-2000: 2000US-0632366.
 PR 21-SEP-2000: 2000US-0234687.
 PR 27-SEP-2000: 2000US-0236359.
 PR 04-OCT-2000: 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI: 2001-488898/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 PT analysing gene expression in human adult liver
 XX
 PS Claim 1: SEQ ID No 9986; 658bp; English.
 XX

XX The invention relates to a single exon nucleic acid probe (SEN) (1) for
 CC measuring human gene expression in a sample derived from human adult
 CC liver, comprising one of 13109 defined nucleotide sequences given in the
 CC specification (or complements/ fragments). The probe hybridises at high
 CC stringency to a nucleic acid molecule expressed in the human adult
 CC liver. (1) may be used for predicting, measuring and displaying gene
 CC expression in samples derived from human adult liver. The genes
 CC identified may be involved in genetic liver diseases such as cirrhosis,
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which
 CC is associated with coronary heart disease. ABS25011-ABS51005 represent
 CC human liver single exon nucleic acid probes of the invention.
 CC Note: The sequence information for this patent does not appear in the
 CC printed specification but was obtained in electronic format directly
 CC from WIPO at http://wipo.int/pub/published/pct_sequences.
 XX

XX Sequence 570 BP: 97 A; 158 C; 213 G; 102 T; 0 other;
 Query Match 39.94; Score 255.2; DB 23; Length 570;
 Best Local Similarity 98.88; Pred. No. 4.3e-46;
 Matches 257; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 340 CCGGCGGCTGAGCTGAGCTGAACCCGACGACGCTTCTTCTGCTGAGACACACAC 394
 Db 311 CAGGCGGCTGAGCTGAGCTGAACCCGACGACGCTTCTTCTGCTGAGACACACAC 370
 QY 400 CATGCTGAGTGTGTCACGCTGACGACATATCTAGAGAGAGAGAGAGAGAGAGAG 454
 Db 371 CATGCTGAGTGTGTCACGCTGACGACATATCTAGAGAGAGAGAGAGAGAGAGAG 430
 QY 460 CTTCCTATATGCTTACGCTCCGAGAAACCTTCGGCTTCTGAGCTACATACATAC 519
 Db 431 CTTCCTATATGCTTACGCTCCGAGAAACCTTCGGCTTCTGAGCTACATACATAC 470
 QY 520 GGCTCGGCTGGAGTGGGGGGCCCGGTGAGGCTTCCAGAGACTTCTGTTCT 579
 Db 491 GGCTCGGCTGGAGTGGGGGGCCCGGTGAGGCTTCCAGAGACTTCTGTTCT 550
 QY 580 GAAGTGAAGTGGCTTCTACCG 599
 Db 551 GAAGTGAAGTGGCTTCTACCG 570

RESULT 13

ABK63807
 ID ABK63807 standard; cDNA: 861 BP.
 XX
 AC ABK63807:
 XX 18-JUN-2002 (first entry)
 XX
 DE Rat sequence differentially expressed in response to a hepatotoxin #1714.
 XX
 KW Rat; ss; hepatotoxic; expressed sequence tag; EST; drug screening;
 KW differential expression; centrilobular necrosis; steatosis.
 XX
 OS Rattus norvegicus.
 XX
 PN W0200210453-A2.
 XX 07-FEB-2002.
 XX 30-JUL-2001: 2001WO-0523872.
 XX
 PR 31-JUL-2000: 2000US-222040P.
 PR 02-NOV-2000: 2000US-244880P.
 PR 11-MAY-2001: 2001US-290025P.
 PR 15-MAY-2001: 2001US-290645P.
 PR 22-MAY-2001: 2001US-292336P.
 PR 06-JUN-2001: 2001US-295798P.
 PR 13-JUN-2001: 2001US-297457P.
 PR 19-JUN-2001: 2001US-298884P.
 PR 09-JUL-2001: 2001US-303459P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Mendrick D, Porter MW, Johnson KH, Castle AL, Flashoff MR;
 XX
 DR WPI: 2002-241625/29.
 XX

XX Predicting toxic effects of compounds or the progression of these toxic
 PT effects by determining the changes in gene expression in tissues of
 PT cells exposed to the toxin and comparing these to gene expression in
 PT unexposed tissues or cells
 XX
 PS Claim 1: Seq ID No 1714; 239bp; English.
 XX

XX The invention relates to methods for predicting toxic effects of
 CC compounds or the progression of these toxic effects by determining the
 CC global changes in gene expression in tissues or cells exposed to the
 CC toxin and comparing these to gene expression in unexposed tissues or
 CC cells. Also included are methods or predicting at least one toxic
 CC effect of a compound or progression of a toxic effect, preferably the
 CC hepatotoxicity of a compound, comprising detecting the level of
 CC expression in a tissue or cell sample exposed to the compound of two or

CC dermatomyositis and polymyositis, myopathy, myasthenia gravis, and mental disorders (e.g. Tourette's syndrome). cDNA sequences AB199746 - AB199929
 CC represent human secretory polynucleotides of the invention.
 XX

Sequence 1910 BP; 588 A; 399 C; 382 G; 539 T; 2 other:

Query Match 33.7%; Score 215.4; DB 24; Length 1910;
 Best Local Similarity 74.0%; Pred. No. 2e-37;
 Matches 273; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 130 GGGCCGGCGGATGCCCTCAGACCGGCTTTACAGCAGCGGGGAGCTTCGCGGACCGCTG 189
 DB 6 GCGCCGACCAATCGCGCTGAGAAAGCCCTCAAGCAGCGCGCCGACACCTTCGAAACAAGAGT 65
 QY 190 TAAGAGATACAGACATCGCGACACCGACCCGACAAATCCCGGTGATCATGACG 249
 DB 66 AGAAGATTCGGACTATTTCAGAGCAGCATCCAAACAAATCCCGGTGATTAATAGACG 125
 QY 250 CTACAGGGTGAAGAAGCAGCTGCCGCTCTGACACAGACCAAGTTTGTCCCGACCA 309
 DB 126 ATACAGGGTGAAGAAGCAGCTTCCTGTTCTGATAAACAAAGTTCTTGTACCTGACCA 185
 QY 310 TGTAAACATGAGCAGATGCTGACAGATCATCCGGTGGCGCTGCAGCTGAACCCGACCA 369
 DB 186 TGTAAACATGAGTACGCTCATCAAGATTAATAGAAAGCGCTTACAGCTCAATGCTAATCA 245
 QY 470 GGGCTTCTCTCTGCTGAGAACACAGCAGCATGGTGTGTCATCCGATCGCGGA 429
 DB 216 GGGCTTCTCTCTGTTGTGTAACGAGCAGCATGGTGTGTCATCCGATCGCGGA 305
 QY 490 CATCTACGAGCAGAGAAAGCAGAGCAGCGCTTCTCTATATGTTCTACGCTCCGACCA 489
 DB 306 GGTGATGAGAGTGAAGAAGATGAAGATGATTCGTACATGGTCTATGCTCCGACCA 365
 QY 490 AACCTTCGG 498
 DB 346 GACGTTCCG 374

RESULT 15

AA158816
 ID AA158816 standard; cDNA: 768 BP.

AA158816:

22-OCT-2001 (first entry)

DE Human polynucleotide SEQ ID NO 1019.

XX Human: neotropic; immunosuppressant; cyostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW leukemia; ss.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0552317.

XX 09-JUL-2000; 2000US-0598042.

XX 19-JUL-2000; 2000US-0620312.

XX 03-AUG-2000; 2000US-0653450.

XX 14-SEP-2000; 2000US-0662191.

XX 19-OCT-2000; 2000US-0663036.

XX 29-NOV-2000; 2000US-0727344.

PA (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Aswadi V, Chen R, Ma Y, Qian XB, Ren F, Wang L;
 PI Wang J, Wang Z, Wehrman I, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QH, Zhou P, Goodrich R, Drmanac RT;
 XX

WP1: 2001-442253/47.
 DR P-PSDB: AAM39460.

PT Novel nucleic acids and polypeptides, useful for treating disorders
 PI such as central nervous system injuries.

PS Claim 1; SEQ ID NO 1019; 10078BP; English.

XX The invention relates to human nucleic acids (AA157798-AA161464) and
 CC the encoded polypeptides (AAM39462-AAM42213) with neotropic,
 CC immunosuppressant and cyostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localized neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

XX Sequence 768 BP; 236 A; 180 C; 175 G; 177 T; 0 other:

Query Match 34.6%; Score 215; DB 22; Length 768;
 Best Local Similarity 74.1%; Pred. No. 2.2e-37;
 Matches 272; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 132 CCGGCGGATGGCTCGAATCGGCTTTCAGACAGCGCGGAGCTTCGGGACGCTGTA 191
 DB 101 CCGGATGATGGCTGGCGGAAAGAGCTTTCAGACAGCGCGGAGCTTTCAGAAAGAGT 160
 QY 192 AGAGGATGAGCAGATCGGATGAGCAGAGCGGAGGAGGAGGAGGAGGAGGAGGAG 251
 DB 161 AAGATGCTCGAGCTTATTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 220
 QY 252 ACAAGGATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 311
 DB 221 ACAAGGATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 280
 QY 312 TCAACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 371
 DB 281 TCAACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 340
 QY 372 CCTTCTTCTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 431
 DB 341 CCTTCTTCTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 400
 QY 432 TCTACGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 491
 DB 401 TGTATGAGAGTGAAGAAGATGAAGATGATTCCTGATGATGATTCCTGATGATGATGAT 460
 QY 492 CCTTCGG 498
 DB 461 CGTTCGG 467

Search completed: August 15, 2003, 08:13:49
 Job time : 261 secs

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OM nucleic - nucleic search, using sw model

Run on: August 15, 2003, 08:06:39 : Search time 74 Seconds
(without alignments)
3817.368 Million cell updates/sec

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Perfect score: 640
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2-6/ptodata/1/lna/5B_COMB.seq:*
3: /cgn2-6/ptodata/1/lna/6A_COMB.seq:*
4: /cgn2-6/ptodata/1/lna/6B_COMB.seq:*
5: /cgn2-6/ptodata/1/lna/PCTUS_COMB.seq:*
6: /cgn2-6/ptodata/1/lna/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	640	100.0	640	2	US-08-805-117-2
2	640	100.0	640	3	US-09-199-838-2
3	215	33.6	768	4	US-09-620-312D-707
4	214.4	33.5	2199	4	US-09-708-725A-3
5	108.4	16.9	201	4	US-09-708-725A-1
6	53.6	8.4	939	4	US-09-252-991A-4537
7	53.6	8.4	1317	4	US-09-252-991A-4950
8	53.6	8.4	1932	4	US-09-252-991A-4998
9	49.8	7.8	1764	4	US-09-252-991A-1709
10	49	7.7	2038	4	US-09-620-312D-597
11	47.2	7.4	519	4	US-09-702-705-78
12	47.2	7.4	519	4	US-09-736-457-78
13	47	7.3	1950	3	US-08-911-851-14
14	47	7.3	1950	3	US-09-479-409-14
15	47	7.3	1950	4	US-09-479-453-14
16	47	7.3	17612	3	US-08-911-851-29
17	47	7.3	17612	3	US-09-479-409-29
18	47	7.3	17612	4	US-09-479-453-29
19	45.6	7.1	477	2	US-08-665-647-12
20	45.6	7.1	990	4	US-09-252-991A-11517
21	45.6	7.1	2166	4	US-09-252-991A-11722
22	45.4	7.1	906	4	US-09-252-991A-1857
23	44.8	7.0	1575	4	US-09-252-991A-11212
24	44.8	7.0	1620	4	US-09-252-991A-11146
25	44.8	7.0	2472	4	US-09-252-991A-11043
26	44.8	7.0	45272	1	US-08-614-770A-1
27	44.2	6.9	1995	1	US-08-425-069-3

28	44.2	6.9	1995	2	US-08-417-844B-3	Sequence 3, Appl 1
29	43.4	6.8	3318	4	US-09-593-589-3	Sequence 3, Appl 1
30	42.8	6.7	1659	4	US-09-084-351-3	Sequence 3, Appl 1
31	42.8	6.7	1659	3	US-09-084-352-3	Sequence 3, Appl 1
32	42.8	6.7	3466	3	US-09-084-351-1	Sequence 1, Appl 1
33	42.8	6.7	3466	3	US-09-084-352-1	Sequence 1, Appl 1
34	42.2	6.6	2433	4	US-09-620-312D-830	Sequence 830, App
35	42.2	6.6	2598	4	US-09-417-197-110	Sequence 110, App
36	42.2	6.5	2616	4	US-09-417-197-108	Sequence 108, App
37	41.8	6.5	777	4	US-09-252-991A-6204	Sequence 6204, App
38	41.8	6.5	1836	4	US-09-252-991A-6042	Sequence 6042, App
39	41.8	6.5	1911	4	US-09-252-991A-6258	Sequence 6258, App
40	41.8	6.5	35081	2	US-08-752-760A-1	Sequence 1, Appl 1
41	41.6	6.5	942	4	US-09-252-991A-5840	Sequence 5840, App
42	41.6	6.5	1503	4	US-09-464-702A-33	Sequence 33, Appl 1
43	41.6	6.5	1503	4	US-09-464-135-33	Sequence 33, Appl 1
44	41.6	6.5	2007	4	US-09-252-991A-5770	Sequence 5770, App
45	41.6	6.5	3627	4	US-09-792-594-3	Sequence 3, Appl 1

ALIGNMENTS

RESULT 1
US-08-805-117-2
Sequence 2, Application US/08805117
Patent No. 5955312
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Goll, Surya K.
TITLE OF INVENTION: NOVEL MICROTUBULE-ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/805,117
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: IF-0211 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 640 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: THYRNTO3
CLONE: 1441378
US-08-805-117-2
Query Match 100.0% Score 640; DB 2; Length 640;
Best Local Similarity 100.0% Pred. No. 1,96-134;
Matches 640; Conservative 0; Mismatches 0; Gaps 0;

OY	1	CTCCCGCAGCCGACGCGCGCTGCTCAGAGCGCAGCCCGGAGCGCTTGGAGCGGAGAGCGC	60
Db	1	CTCCCGCAGCCGACGCGCGCTGCTCAGAGCGCAGCCCGGAGCGCTTGGAGCGGAGAGCGC	60
OY	61	GGAGCCCGGAGCCCGCCAAACCGCAGACACATCCCGCGCCCGCAGAGCCCGGCGCTGCGC	120
Db	61	GGAGCCCGGAGCCCGCCAAACCGCAGACACATCCCGCGCCCGCAGAGCCCGGCGCTGCGC	120
OY	121	GCCCGAGCGCGCGCGCGCGATGCGCTCCACACCGCGCTTTCAGACAGCGCGGAGCTTCCG	180
Db	121	GCCCGAGCGCGCGCGCGCGATGCGCTCCACACCGCGCTTTCAGACAGCGCGGAGCTTCCG	180
OY	181	CGACCGCTGTAAAGAGGTACAGACAGATCCGCGACCGACCGCCAGCAAAATCCCGGTGAT	240
Db	181	CGACCGCTGTAAAGAGGTACAGACAGATCCGCGACCGACCGCCAGCAAAATCCCGGTGAT	240
OY	241	CATCGAGCGCTACAAAGGGTGAGAGCAGCTGCCGCTCTGTGACAAAGACCAAGTTTGGT	300
Db	241	CATCGAGCGCTACAAAGGGTGAGAGCAGCTGCCGCTCTGTGACAAAGACCAAGTTTGGT	300
OY	301	CCCGGACCATGTCAACATGAGGAGTTGGTCAAGATCATCCGCGCGCGCTGTAGCTGAA	360
Db	301	CCCGGACCATGTCAACATGAGGAGTTGGTCAAGATCATCCGCGCGCGCTGTAGCTGAA	360
OY	361	CCCCACGAGCGCTTCTCTCTGCTGGTGAACCGACGACAGCATGGTGAAGTGTGTCAGGC	420
Db	361	CCCCACGAGCGCTTCTCTCTGCTGGTGAACCGACGACAGCATGGTGAAGTGTGTCAGGC	420
OY	421	CATCGCGGACATTCAGAGCAGAGAAAGCAGAGAGCGGCTTCTCTATATGGTCTACGC	480
Db	421	CATCGCGGACATTCAGAGCAGAGAAAGCAGAGAGCGGCTTCTCTATATGGTCTACGC	480
OY	481	CTCCCGAGAAACCTTCGGCTCTGAGCAGAGTAGGGGGCTCGGCGCTGGAGTGGGG	540
Db	481	CTCCCGAGAAACCTTCGGCTCTGAGCAGAGTAGGGGGCTCGGCGCTGGAGTGGGG	540
OY	541	GGCCCGGTCAGGCGCTTCGTGAGCCAGCATGAGGGGGCTCGGCGTGGGAGTGGGG	600
Db	541	GGCCCGGTCAGGCGCTTCGTGAGCCAGCATGAGGGGGCTCGGCGTGGGAGTGGGG	600
OY	601	GGTGGGCTGGGCGAGCATGTGCCCGCTAGTCAGAGGGCA	640
Db	601	GGTGGGCTGGGCGAGCATGTGCCCGCTAGTCAGAGGGCA	640
RESULT 2			
US-09-199-838-2			
Sequence 2, Application US/09199838			
Patent No. 6280733			
GENERAL INFORMATION:			
APPLICANT: Hillman, Jennifer L.			
APPLICANT: Goli, Surya K.			
TITLE OF INVENTION: NOVEL MICROTUBULE-ASSOCIATED PROTEIN			
NUMBER OF SEQUENCES: 3			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Juncyte Pharmaceuticals, Inc.			
STREET: 3174 Porter Drive			
CITY: Palo Alto			
STATE: CA			
COUNTRY: USA			
ZIP: 94304			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Diskette			
COMPUTER: IBM Compatible			
OPERATING SYSTEM: DOS			
SOFTWARE: FastSeq for Windows Version 2.0			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/199,838			
FILING DATE:			
CLASSIFICATION:			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US/08/805,117			

```

: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: Pf-0211 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-855-0555
: TELEFAX: 415-845-4166
:
: INFORMATION FOR SPO ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 640 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: THYNOT03
: CLONE: 1441378
:
: US-09-199-838-2
:
: Query Match 100.0%; Score 640; DB 3; Length 640:
: Best Local Similarity 100.0%; Pred. No. 1,9e-134;
: Matches 640; Conservative 0; Mismatches 0; Indels 0; Gaps 0
:
: QY 1 CTCCTCCGAGCCGCGAGCCGCGCTGCTCAGCGCGAGCCCGGAGCCCTTGAGCGAGCGCG 60
: Db 1 CTCCTCCGAGCCGCGAGCCGCGCTGCTCAGCGCGAGCCCGGAGCCCTTGAGCGAGCGCG 60
:
: QY 61 GAGAGCCCCGGAGCCCCCAACCGCGAGACATCCCCGGGCCCCGAGAGCCCGGCTCGC 120
: Db 61 GAGAGCCCCGGAGCCCCCAACCGCGAGACATCCCCGGGCCCCGAGAGCCCGGCTCGC 120
:
: QY 121 GCCCAGCCGCGGCGCCGCGCGATCCCTTCAGACCGCGCTTTCGAAGAGCGCGGAGCTTCG 180
: Db 121 GCCCAGCCGCGGCGCCGCGCGATCCCTTCAGACCGCGCTTTCGAAGAGCGCGGAGCTTCG 180
:
: QY 181 CGAGCCCTGTAAAGAGAGTACAGCAATCCGCGACAGACCCGACCAAAATCCGGTGAT 240
: Db 181 CGAGCCCTGTAAAGAGAGTACAGCAATCCGCGACAGACCCGACCAAAATCCGGTGAT 240
:
: QY 241 CATCGAGCGCTACAAAGGTGAGAAAGACAGCTGCCGCTCTGGACAAAGCAAGTTTGGT 300
: Db 241 CATCGAGCGCTACAAAGGTGAGAAAGACAGCTGCCGCTCTGGACAAAGCAAGTTTGGT 300
:
: QY 301 CCGGAGCAATGTCAACATATAGCGAATTTGGTCAAGATCATCCGCGCGCTCGAGCTGAA 360
: Db 301 CCGGAGCAATGTCAACATATAGCGAATTTGGTCAAGATCATCCGCGCGCTCGAGCTGAA 360
:
: QY 361 CCGCAGCAGAGGCTTCTTCGCTGCTGTAACAGACAGATGGTGAGTGTGTACAGCC 420
: Db 361 CCGCAGCAGAGGCTTCTTCGCTGCTGTAACAGACAGATGGTGAGTGTGTGTACAGCC 420
:
: QY 421 CATCGCGGAGCATCTACAGAGCAGAAAGAGAGAGAGCGCTTCCCTATATGTGTTACG 480
: Db 421 CATCGCGGAGCATCTACAGAGCAGAAAGAGAGAGAGCGCTTCCCTATATGTGTTACG 480
:
: QY 481 CTCCTCCAGAAACCTTCGCTTCTGAGCCAGCATGTAAGGGGAGCTCGGCTGGAGTGGGG 540
: Db 481 CTCCTCCAGAAACCTTCGCTTCTGAGCCAGCATGTAAGGGGAGCTCGGCTGGAGTGGGG 540
:
: QY 541 GGGCCCGGTGACAGGCTTCGCGCAGAGAGTTCCTGATCTGAACGTGACCTGCTACCGT 600
: Db 541 GGGCCCGGTGACAGGCTTCGCGCAGAGAGTTCCTGATCTGAACGTGACCTGCTACCGT 600
:
: QY 601 GGTGGGCTGGGAGGAGCATGTGCCCTCAATGTCAGAGGGA 640
: Db 601 GGTGGGCTGGGAGGAGCATGTGCCCTCAATGTCAGAGGGA 640
:
: RESULT 3
: US-09-620-312D-707
: Sequence 707, Application us/09620312D
: Patent No. 6569662

```



```

: GENERAL INFORMATION:
: APPLICANT: Tang, Y. Tom
: APPLICANT: Liu, Chenghua
: APPLICANT: Asundi, Vinod
: APPLICANT: Zhang, Jie
: APPLICANT: Ren, Feiyan
: APPLICANT: Chen, Rui-hong
: APPLICANT: Zhao, Qing A.
: APPLICANT: Wehrman, Tom
: APPLICANT: Xue, Aidong J.
: APPLICANT: Yang, Yonghong
: APPLICANT: Wang, Jian-Rui
: APPLICANT: Zhou, Ping
: APPLICANT: Ma, Yunqiang
: APPLICANT: Wang, Dunrui
: APPLICANT: Wang, Zhimei
: APPLICANT: John Tillinghast
: APPLICANT: Drmanac, Radoje T.
: TITLE OF INVENTION: No. 656962e1 Nucleic Acids and
: TITLE OF INVENTION: Polypeptides
: FILE REFERENCE: 784CIP2B
: CURRENT APPLICATION NUMBER: US/09/620,312D
: CURRENT FILING DATE: 2000-07-19
: PRIOR APPLICATION NUMBER: 09/552,317
: PRIOR FILING DATE: 2000-04-25
: PRIOR APPLICATION NUMBER: 09/488,725
: PRIOR FILING DATE: 2000-01-21
: NUMBER OF SEQ ID NOS: 1105
: SOFTWARE: Pf_genes Version 1.0
: SEQ ID NO 707
: LENGTH: 768
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (109)..(486)
: US-09-620-312D-707

Query Match      33.6%: Score 215: DB 4: Length 768:
Best Local Similarity 74.1%: Pred. No. 1.5e-39:
Matches 272: Conservative 0: Mismatches 95: Indels 0: Gaps 0:

QY 132 CCGCGGGATGCGCTCAGACGCGGCCCTTTCAGACGCGCGAGGCTTGCGCGACGGCTGTA 191
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 101 CCGCGACCATGCGCTCGGAGAGACCTTCAAGCAGCGCGGACCTTCGAACAAAGAGTAG 160

QY 192 AGGAGGTACAGACATCCGCGAGCAGACCCGACGAAATCCGGGTATCATCGAGCGCT 251
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 161 AAGATGTCCGACTTATTTCGAGAGCGAGCATCCACCAAAATCCCGGTATATAGACGAT 220

QY 252 ACAAGGTTGAGAACGACCTGCGCTGCTGCGACAGACCAAGTTTGTGCGCGGAGCATG 311
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 221 ACAAGGTTGAGAACGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 280

QY 312 TCAACATGAGCGAGTGTGTCAAGATCATCCGCGCGCGCTGCGACGTAACCCGACGAG 371
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 281 TCAACATGAGTGTGAGCTCATAGATTAATTAGAAAGCGCGTTACAGCTCATGTATACAG 340

QY 372 CCTTCTCTCTGCTGTGTAACGACGACGATGTGTGTCCAGCGCCATCGCGGACA 431
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 341 CCTTCTCTCTGCTGTGTAACGACGACGATGTGTGTCCAGCGCCATCGCGGAGG 400

QY 432 TCTACGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 491
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 401 TGTATGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 460

QY 492 CCTTGGG 498
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Db 461 CGTTGGG 467

RESULT 4
US-09-708-725A-3
```

```

: Sequence 3, Application US/09708725A
: Patent No. 6489456
: GENERAL INFORMATION:
: APPLICANT: LADUNGA et al.
: TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: CL000842
: CURRENT APPLICATION NUMBER: US/09/708,725A
: CURRENT FILING DATE: 2000-11-09
: PRIOR APPLICATION NUMBER: 60/243,428
: PRIOR FILING DATE: 2000-10-27
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 2199
: TYPE: DNA
: ORGANISM: Human
: US-09-708-725A-3

Query Match      33.5%: Score 214.4: DB 4: Length 2199:
Best Local Similarity 68.5%: Pred. No. 2.5e-39:
Matches 296: Conservative 0: Mismatches 136: Indels 0: Gaps 0:

QY 67 CCGGAGTCCCGCAAAATCGTATACATCCCGCGCGCGGAGAGCCCGCGTGTGCGCGAG 126
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 750 CCGGAGTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 809

QY 127 CCGGAGTCCCGCGAATGCGCGTATGAGACCGCGCGCTTTGAAGCAGCGCGGAGCTTTGCGGAGCG 186
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 810 AGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 869

QY 187 CTGTAAAGGAGGTACAGAGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 246
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 870 AGTAAAGAGTGTGACCTTATTTGAGAGCGAGATTCGCAAAATCCCGCGGTATATAGTA 929

QY 247 GCGCTACAGAGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 306
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 930 AGCATACAGAGGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 989

QY 307 CCATGTCAACATGAGCGAGTGTGTCAABATATCCGCGCGCGCGCTGCAACATGAGAG 366
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 990 CCATGTCAACATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1049

QY 367 GCAGCGCTTCTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 426
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1050 TCAGGCGCTTCTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1109

QY 427 GGCATCTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 486
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1110 AGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1159

QY 487 GGAACCTTGGG 498
   ||||| |||||
Db 1170 GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1181

RESULT 5
US-09-708-725A-1
: Sequence 1, Application US/09708725A
: Patent No. 6489456
: GENERAL INFORMATION:
: APPLICANT: LADUNGA et al.
: TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: CL000842
: CURRENT APPLICATION NUMBER: US/09/708,725A
: CURRENT FILING DATE: 2000-11-09
: PRIOR APPLICATION NUMBER: 60/243,428
: PRIOR FILING DATE: 2000-10-27
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0
```


US-09-252-991A-4998/C
: Sequence 4998, Application US/09252991A
: Patent No. 6551795
: GENERAL INFORMATION:
: APPLICANT: Marc J. Rubenfield et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
: FILE REFERENCE: 107196.136
: CURRENT APPLICATION NUMBER: US/09/252,991A
: PRIOR FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBER: US 60/094,190
: NUMBER OF SEQ ID NOS: 33142
: SEQ ID NO 4998
: LENGTH: 1932
: TYPE: DNA
: ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4998

Query Match 8.4%; Score 53.6; DB 4; Length 1932;
Best Local Similarity 45.3%; Pred. No. 0.0019;
Matches 194; Conservative 0; Mismatches 234; Indels 0; Gaps 0;

QY 57 GCGCGAGACCCCGGAGCCCAAAACCGGAGACATCCCGCGCGCCGAGAGCCCGCCCT 116
DB 1025 GCGCCGAGTGGCGATCCCGGTACTGAGCTCCGATCCCGCGCGCCGAGAGCCCG 966
QY 117 GCGCGCCGAGCGCGCGCCCGCGGATGCCCTGAGACCGGCGCTTCAAGCAGCGCGGAGCT 176
DB 965 AGCGGATCCCGCGCGCGGATGCCGCTGTGAGAGAGCTCAAGCAGCGCGGATCCGCA 906
QY 177 TCGCGGACCGGTGTAGAGAGGTAGAGAGATCCCGGAGCAGCCCGCAAAATCCCGG 236
DB 905 TCGCGTCCGCGCGCGCGCCCTCTTATACGATGAGGAGGAGCAAGCTGAGGAGATCC 846
QY 217 TGATATGAGCGCGGTACAGAGGTGAGAGAGTCCCGCTGCGGAGAGCAAGATTTT 296
DB 845 TGCTACGCGAGGAGTCCAGCCCGAGCATCCAGATGAGCTGAGCAGAGCCGCTTCGAG 786
QY 297 TGTCCCGGAGCATGTCAACATGAGCGAGTTGCTCAAGATATCCGCGCGCGCTCGAGC 356
DB 785 TGGAGCAAGCGCCAGAGCGGAGCGGAGCGCCGCTGCGCGCTCGAGCGCTCGAGC 726
QY 357 TGAACCGCAGCGAGCGCTTCTCTCTGCTGTGAGACCGACAGCATGTGAGTGTCCA 416
DB 725 TGTGCGCGCGCGCTTCCAGCGGCTGAGCATGAGCGGAGTGTGAGCAGCATGCGCA 666
QY 417 CGCCCATCGCGAGCATCTACGAGGAGAGAGAGAGAGCGGCTTCTATATGCTCT 476
DB 665 TGTGCTGGAAGCAACGAGCTGCTGATGATCCGCGGAACTCAAGCTGAGTGGCA 606
QY 477 AGCGCTTC 484
DB 605 GCGGCTTC 598

RESULT 9
US-09-252-991A-1709
: Sequence 1709, Application US/09252991A
: Patent No. 6551795
: GENERAL INFORMATION:
: APPLICANT: Marc J. Rubenfield et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
: FILE REFERENCE: 107196.136
: CURRENT APPLICATION NUMBER: US/09/252,991A
: PRIOR FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27

: NUMBER OF SEQ ID NOS: 33142
: SEQ ID NO 1709
: LENGTH: 1764
: TYPE: DNA
: ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1709

Query Match 7.8%; Score 49.8; DB 4; Length 1764;
Best Local Similarity 44.3%; Pred. No. 0.013; Indels 1; Gaps 1;
Matches 245; Conservative 0; Mismatches 307;

QY 17 GCGCGTCTCAGCGCGAGGCTGTGAGAGCCCTTGAGTGGGAGGCTGCGAGAGCGGCTA 76
DB 681 GCGCGAGCGAGTGTCTGATGAGAGCTGCTGTGCGGGGTGTGCGCGTCCGCGCGCT 740
QY 77 CAACCGCAGACACATCCCTGCGCGCGAGAGCTGCGGCTGTGCGCGCT-AGCGGCTGCG 145
DB 741 TCGACCGCCATCCCTCGCGCGAGCAACCGCGGCTTACCTGATTAACCAAGTAAAGTA 809
QY 136 CGCGATGCCCTGACAGCGCGCTTTCAGAGAGCGGTGAGAGCTTCCGCGAGCGCTTGAAGTA 195
DB 801 CGCGATGCTGACAGAGCTGCTGTGTGCGCGCTTCTGCGCTGCGCGAGTGGGCTGCG 860
QY 196 GGTACAGCAGATCGCGAGCAATACCGCAGCAAAATCCCGGTGATCATGCAATGTAACA 255
DB 861 CGAGCGTACCGCGCTGAGCGTGTGAGTGTGAGCGCGCGAGCGAGTGAAGTGTGAGT 920
QY 256 GAGTGAAGAGTGTGCGCGTGTGAGCAAGATTAAGTTTGTGCGGAGTGAATGTA 415
DB 921 GTCGCGCGTGTGAGCGTGTGAGCAATGCAATGCAAGTGTGAGTGTGAGTGTGAGT 980
QY 316 CAIAGCGAGTGTGAGCAATGATGCGCGGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 475
DB 981 GAGCGGTATGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1040
QY 376 CTCTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 435
DB 1041 GATCGCGCGCGTCAAGCGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1106
QY 436 CGAGCAGAGAGAGAGCGAGGAGTGTGCTCTATATGCTGTGAGCTTCCAGAGAACCT 495
DB 1101 GCTGAGTGTGAGCGCGGAGCTGTGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1160
QY 496 CGCGTGTGAGCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 555
DB 1161 GAGCTGAGTGTGAGCGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1220
QY 556 CTGCGCAGAGAG 568
DB 1221 CTGCGCGCAGAG 1233

RESULT 10
US-09-620-312D-597
: Sequence 597, Application US/09620312D
: Patent No. 6569662
: GENERAL INFORMATION:
: APPLICANT: Tang, Y. Tom
: APPLICANT: Liu, Chenghua
: APPLICANT: Asundi, Vinod
: APPLICANT: Zhang, Jie
: APPLICANT: Ren, Feiyun
: APPLICANT: Chen, Rui-hong
: APPLICANT: Zhao, Qing A.
: APPLICANT: Weinman, Tom
: APPLICANT: Xue, Aidong J.
: APPLICANT: Yang, Yonghong
: APPLICANT: Wang, Jian-kui
: APPLICANT: Zhou, Ping
: APPLICANT: Ma, Yundong
: APPLICANT: Wang, Dunfui
: APPLICANT: Wang, Zhiwei
: APPLICANT: John Tiliudast

QY 122 CCCAGCCGGGCCCCCGGATGCCCTCAGACCCGGGCTTTCAAGCAGCGGGAGCTTCCGC 181
Db 38 CGCGGCTTGCGACCTCGACCAAGCTCTGGACATGTCTTACGAGCGATGATCAGCTGTAC 97
QY 182 GACCGGTGTAAAGAGGTACAGCAGATCCGGAGCCAGACCCACAGCAAAATCCCGGTATC 241
Db 98 AGTCCGCGCCAGCGCGGCTGTAAACCGGGGCTGCGGCGGAAGCAGCACTTCCCTGCTG 157
QY 242 ATCAGCGGTACAAGGGGTGAGAACGAGCTGCGCCCTCCGAGCAAGACCAATTTTGGTTC 301
Db 158 AAGCGCTTGCGCAAGGCCAAGAAAGAGAGCGCGCCCATGTGAGGAAGCCGGAAGTGTGTAG 217

Db 826 CGCCTACGCGACGAGCCCAAGACCTTGCCCGGACACCTTCCGAGGGG 885
 QY 242 ATCGAGCGCTTACAGAGGTGAGAGAGAGCTGCCGCTTGGAGACCAAGTTTGTGTC 301
 Db 886 TTGAAGACCGCGAGGCTGTGCGGAGCGCCGAGAGACCGGAGAACATCTCTGATC 945
 QY 302 CCGGACCATGTACATGAGCGAGTGTGCAAGATCATCCGGCCCGCTGAGCTGANC 361
 Db 946 CGCGCGGAGAGAGCTCAATCCCTGCTGCTGCGGAGATCCGACACCGCTGCGGAGC 1005
 QY 362 CCCAGCAGGCGCTTCTTCTGCTGCTGGAACAGCAGCATGTGTGATGTGTCACAGGCC 421
 Db 1006 CTGAGAGGAATGTGTCGCAACCTCGACGTGCGCGCGCCGAGTGATGTGAGGCGGCC 1065
 QY 422 ATCGCGGACATCTACAG 481
 Db 1066 ATCGTGAATATCTCCGGGAGATCAAGCAGCGCCCTCGGCGGTGCAATGGGCGGTGATGCC 1125
 QY 482 TCCCAGGAACCTTGGGCTTCTGAG 506
 Db 1126 CGCGGCGGACCGCGGCTCGCG 1150

RESULT 15

US-09-479-453-14

; Sequence 14, Application US/09479453

; Patent No. 6313283

; GENERAL INFORMATION:

; APPLICANT: Geritise, Gijdsbert

; APPLICANT: Quax, Wilhelmus J.

; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED

; TITLE OF INVENTION: EXPRESSION LEVELS

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESS: Genencor International

; STREET: 925 Page Mill Road

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304-1013

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: PASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/479,453

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/911,853

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Glaister, Debra J

; REGISTRATION NUMBER: 33,888

; REFERENCE/DOCKET NUMBER: GC361-2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-846-7620

; TELEFAX: 650-845-6504

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1950 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-09-479-453-14

Query Match

Best Local Similarity 7.3%; Score 47; DB 4; Length 1950;

Matches 203; Conservative 0; Mismatches 240; Indels 2; Gaps 1;

QY 64 GCCCGGAGCCCGCAACCGAGACACATCCCGCGCCGAGAGCCCGGCTGGCG--G 121
 Db 706 GCCGACGCGCGCACCAACCGCTGATCTCTCGCGCGCGCGCGCGCGCGCGCGCTG 765

QY 122 CCCAGCCGCGCCCGCGCGATGCGCTTCAAGACGCGGAGCTTTCGCC 181
 Db 766 GCCAACCTGCGCGCGCTGCGTGAACATCCCGACACCGCTTGGCCCAATCCGGGTAATT 825
 QY 182 GACCGCTGTAAAGAGGTACAGAGATCCGCGACAGCAGCAGCAAAATCCGGTATC 241
 Db 826 CGCCTACGCGACAGCGAGCGCCAAAGAGCGCTGCGCGAGACCTTGGGACATCTCCGAGGG 885
 QY 242 ATCGAGCGCTTACAGAGGTGAGAGAGAGCTGCCGCTTCTGACAAAGCAAGTTTGTGTC 301
 Db 886 TTGAAGACCGCGAGAGGTGTGCGAGAGCGCCAGCAGCAGCAACCCAGAACATCTGATC 945
 QY 302 CCGGACCATGTCAACATGAGAGAGTGTGCAAGATCATCCGGCCCGCTGAGCTGANC 361
 Db 946 CGCGCGAGAGAGCTCAATCCCTGTGCTGTGCGGATCCGAGACAGCTGGCGAGC 1005
 QY 362 CCCAGCAGGCGCTTCTTCTGCTGTGAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 421
 Db 1006 CTGAGAGGAATGTGTCGCAACCTCGACGTGCGCGCGCCGAGTGATGTGAGGCGGCC 1065
 QY 422 ATCGCGGACATCTACAG 481
 Db 1066 ATCGTGAATATCTCCGGGAGATCAAGCAGCGCCCTCGGCGGTGCAATGGGCGGTGATGCC 1125
 QY 482 TCCCAGGAACCTTGGGCTTCTGAG 506
 Db 1126 CGCGGCGGACCGCGGCTCGCG 1150

Search completed: August 15, 2003, 09:32:03
 Job time : 76 secs

OY	299	TTCCCGGAGCACATGTACAATAGAGCAGTGGTCAGATCATCCGGCCGCGTCAAGCTG	358
Db	333	GTCCCGGACCATGTACAATGAGCGAGTGGTCAGATCATCCGGCCGCGTCAAGCTG	392
OY	359	AACCCACAGCAGGCGCTTCTCTCTGGTGGTGAACACAGCAGCATGGTGAATGTGTCCAG	418
Db	393	AACCCACAGCAGGCGCTTCTCTCTGGTGGTGAACACAGCAGCATGGTGAATGTGTCCAG	452
OY	419	CCCATCGGCGACATCTACGAGCAGGAGAAAGACGAGGCGCTTCTCTATATGATCTAC	478
Db	453	CCCATCGGCGACATCTACGAGCAGGAGAAAGACGAGGCGCTTCTCTATATGATCTAC	512
OY	479	GCCTCCACAGAAACCTTGGCGCTTCTTGAGCAGCAGTAGGGGGCTTGCGCTGGGAATCG	538
Db	513	GCCTCCACAGAAACCTTGGCGCTTCTTGAGCAGCAGTAGGGGGCTTGCGCTGGGAATCG	572
OY	539	GGGGCGCCGGGTCAGGCGCCTGCCCAAGAGACCTTGTTTCTTAACCTGAGCTGCTTACC	598
Db	573	GGGGCGCCGGGTCAGGCGCCTGCCCAAGAGACCTTGTTTCTTAACCTGAGCTGCTTACC	632
OY	599	GTGGTGCGCTGGGACAGCATGTGGCCCCCTTAGTCAAGAGGCA	640
Db	633	GTGGTGCGCTGGGACAGCATGTGGCCCCCTTAGTCAAGAGGCA	674

```

RESULT 2
US-10-105-837-707
: Sequence 707, Application US/10105837
: GENERAL INFORMATION:
:   APPLICANT: Tang, Y. Tom
:   APPLICANT: Liu, Chenghua
:   APPLICANT: Asundi, Vinod
:   APPLICANT: Zhao, Qing A.
:   APPLICANT: Dirmanac, Radoje T.
:   TITLE OF INVENTION: Novel Nucleic Acids and
:   TITLE OF INVENTION: Polypeptides
:   FILE REFERENCE: 784CIP2BDIVA
:   CURRENT APPLICATION NUMBER: US/10/105,837
:   CURRENT FILING DATE: 2002-03-21
:   PRIOR APPLICATION NUMBER: 09/620,312
:   PRIOR FILING DATE: 2000-07-19
:   PRIOR APPLICATION NUMBER: 09/552,317
:   PRIOR FILING DATE: 2000-04-25
:   PRIOR APPLICATION NUMBER: 09/488,725
:   PRIOR FILING DATE: 2000-01-21
:   NUMBER OF SEQ ID NOS: 1104
:   SOFTWARE: PL_FL_genes Version 1.0
:   SEQ ID NO 707
:   LENGTH: 768
:   TYPE: DNA
:   ORGANISM: Homo sapiens
:   FEATURE:
:   NAME/KEY: CDS
:   LOCATION: (109)..(486)
:   US-10-105-837-707

```

Query Match	33.6%	Score 215	DB 6	Length 768
Best Local Similarity	74.1%	Pred. No. 8e-44		
Matches 272	Conservative	0	Mismatches 95	Indels 0
			Gaps	0

OY	132	CCCCGGGGATCCCGCACAACGGGCTTTCAGACAGCGGCGAGAGCTTCCGCAACCGCTGA	191
Db	101	CCCCCACCATTCCCGTCGGAGAAGACTTTCACAGCACGGCGCACCTTTTCGAACAAAGTAG	160
OY	192	AGGAGGTACACAGATCCGCGACCAAGCACCAGCAAAATCCGGGTGATCATGAGCGCT	251
Db	161	AAGATGTCCGACTTATTCGAGAAGCAGCATCAACCAAAATCCGGGTGATAAATGAACGAT	220
OY	252	ACAAGGGTGAACAAGCAGCTGCCGCGCCAGCAACAGCAACCAAGTTTGGTCCCGGGAACATG	311
Db	221	ACAAGGGTGAACAAGCAGCTTCTCTGTTCGGATATAAACAAAGTCTCTTGTACCTTGACCAATG	280

OY	312	TCAACATGAGCAGTTGGTCAGANATCATCCGGCGCCGTGGAGCTGAACCCCAGCAG	371
Dd	261	TCACATGATGTAGCTCATCANAGTAATTAGAAGCGCTTACAGCTCAATGCTAATCAG	340
OY	372	CCTTCTCTCTGCTGTGAAACCAGCACGCATGTTGAGTGTCACGCCCATCGCGACA	431
Dd	341	CCTTCTCTCTGTTGGTAGAACGGACACAGCATGTCAGCTGTCCACCAACCATCTCAGAG	400
OY	432	TCTACGACGAGAAAGACGAGAGCGCTTCTCTATATGTGTTACGCTTCCAGGAAA	491
Dd	401	TGTAGAGAGATGAGAAAGATGAATGATTCCTGTACATGGTCTATGCTCCACAGAGA	460
OY	492	CCTTCGG	498
Dd	461	CGTTGG	467

```

RESULT 3
US-10-286-897-1019
; Sequence 1019, Application US/10286897
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/10/286, 897
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US/09/552, 317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US/09/598, 042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US/09/620, 312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US/09/653, 450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US/09/662, 191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US/09/693, 036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US/09/727, 344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7143
; SOFTWARE: pc_fl_genes_b Versions 1.0
; SEQ ID NO 1019
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (109)..(486)
; US-10-286-897-1019

```

Query Match	33.6%	Score	215	DB	6	Length	768
Best Local Similarity	74.1%	Pred	No.	8e-44			
Matches	272	Conservative	0	Mismatches	95	Indels	0
						Gaps	0

QY	132	CCCCGGGAGTACCCCTCAACACCGGCGCTTTCACACAGCGGAGCTTCCGCCACCGCTCTGA	191
Db	101	CCCCGACCATCCCGTCGGAGAAAGACTTTCAGCACGCGCGCACCTTTCGAAACAAGAAGTAG <td>160</td>	160
QY	192	AGGAGGTACACAGATCCGCGACACGACCCAGCAAAATCCCGGTGATCATCGAGCGCT	251
Db	161	AAGATGTCCGACTTATTTCGAGAGCAGCATCCACCAAAATCCCGGTGATTAATAGAACGAT	220
QY	252	ACAAGGCTGAGAGCAGCTGCCTCTCTGACACAAGACCAAGTTTTTGGTCCCGGACCATG	311
Db	221	ACAAGGCTGAGAGCAGCTTCTCTGTTCGATTAATAACAAGTCTCTTGACTCGATGCATG	280
QY	312	TCAACATGAGCGAGTTGGTCAAGATCATCCGGCGCGCTTCGACGTGAACCCACCGCAGG	371
Db	281	TCAACATGAGCGACTCATCAAGATAAATTAAGAAAGCGCTTCACGCTCATGTGAATTCAGG	340

OY	372	CCCTTCTTCTGTTGGTGAACCGACAGCATGCTAGTGTGTCCAGCCCATTCGGGACA	431
Db	341	CCCTTTCTCTGTTGGTGAACCGACAGCATGCTAGTGTGTCCAGCCCATTCGGGACA	400
OY	432	TCATACGACAGAGAGAAACGACGAGCGCTTCTCTATATGCTATACGCGCTCCAGGAAA	491
Db	401	TGATAGAGAGTGAAGAAAGTGAAGATGATCTCTGATACATGGCTCTATGGCTCCAGGAGA	460
OY	492	CCCTTCGG	498
Db	461	CGTTTCGG	467

RESULT 4
US-10-25

```

: Sequence 1019, Application US/1025889S8A
:
: GENERAL INFORMATION:
:
: APPLICANT: Hysq Inc
:
: TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
:
: FILE REFERENCE: 784F1PCP
:
: CURRENT APPLICATION NUMBER: US/10/258,898A
:
: CURRENT FILING DATE: 2003-10-20

```

```

# Prior Application Number: 2002-10-09
# Prior Filing Date: 2000-01-21
# Prior Application Number: US09/488,776
# Prior Filing Date: 2000-01-21
# Prior Application Number: US09/552,317
# Prior Filing Date: 2000-04-25
# Prior Application Number: US09/598,044
# Prior Filing Date: 2000-06-20
# Prior Application Number: US09/620,312
# Prior Filing Date: 2000-07-19
# Prior Application Number: US09/653,455
# Prior Filing Date: 2000-08-31
# Prior Application Number: US09/662,191
# Prior Filing Date: 2000-09-14
# Prior Application Number: US09/693,036
# Prior Filing Date: 2000-10-19
# Prior Application Number: US09/727,344
# Prior Filing Date: 2000-11-29
# Number of SEQ ID NOS: 7143
SOFTWARE: pF_FL_genies_b Versions 1.0
SEQ ID NO 1019

```

```

; LENGTH: 768
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (109)..(486)
US-10-258-898A-1019

```

Query Match 33.68; Score 215; DB 6; Length 768;

Best Local Similarity 4.18; Pred. No. 8e-44;
Matches 272; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

[illegible][illegible]

RESULT 5
US-10-286-897-4591/c

; Sequence 4591, Application US/10286897

```

; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 7841Pct
; CURRENT APPLICATION NUMBER: US/10/266,897
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US/09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US/09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US/09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US/09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US/09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US/09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US/09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7143
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 4591
; LENGTH: 2309
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-286-897-4591

```

Query Match	33.6%; Score 215; DB 6; Length 2309;
-------------	--------------------------------------

Matches	272	Conservative	0	Mismatches	95	Indels	0	Gaps	0
Best Local Similarity 74.18; Pred. No. 1.1e-43;									

[illegible]

```

RESULT 6
US-10-258-898A-4591/c
; Sequence 4591, Application US/10258898A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/10/258, 898A
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552, 317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598, 042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620, 312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653, 450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662, 191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693, 036
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US09/727, 344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7143
; SOFTWARE: pl_FL_genes_b Versions 1.0
; SEQ ID NO 4591
; LENGTH: 2309
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-258-898A-4591

Query Match          33.6%; Score 215; DB 6; Length 2309;
Best Local Similarity 74.1%; Pred. No. 1,le-43;
Matches 272; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

OY      132  CCCGGCGATCCCTCAGACCGGCGCTTTCAAGCAGCGGGAGGCTTCGCCGACCGCTGTA 191
DB      2225  CCGGACCATCCCGCGGAGAAGACCTTCAAGCAGCGCGGACCTTCGACAAAGAGTAG 2166
OY      192  AGAGGCTACACAGATCCGGGACGACGACCCGAGAAATCCGGTGATCGACGGCT 251
DB      2165  AAGATGTCGACTTATTTGAGAGCGACGATCCAAACCAATCCGGTGATATAGACGAT 2106
OY      252  ACAAGGGTGAAGACGAGCTGCCGCTCTGCAACAAGACCAGCTTTTGGTCCCGACCATG 311
DB      2105  ACAAGGGGAGAAGACGAGCTTCTGTTGATTAATAACAAAGTCTCTTACCTGACCATG 2046
OY      312  TCAACATGAGGAGATGGTCAAGATCATCCGGCGCGCTCAGCTGAGACCCACGACGAG 371
DB      2045  TCAACATGAGAGCTCATCAAGATTAATTAAGAAGCGGCTTACAGCTCAATCTATATGAG 1986
OY      372  CCTTCTTCCTCTGCTGATGACACGACGACATGATGATGTCATCCACCGCCATCGGGGACA 431
DB      1985  CCTTCTTCCTGTTGGTGTGACGAGACACGACATGATGATGAGGCTTCCACACCAATTCAGAGG 1928
OY      432  TCTACGAGCAGAGAGAAACAGCAGGCGCTTCTCTATATGATGTATACGCTCCAGGAAA 491
DB      1925  TGTATGAGAGTGAGAGAAAGATGAAGATGATTCCTGTATACATGTCATGCTCCAGAGAGA 1866
OY      492  CCTTCGG 498
DB      1865  CGTTGCG 1859

```

```

: APPLICANT: Tang, Y. Tom et al
: TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
: FILE REFERENCE: 21272-029
: CURRENT APPLICATION NUMBER: US/10/293,244
: CURRENT FILING DATE: 2002-11-12
: PRIOR APPLICATION NUMBER: Not yet Assigned
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: 09/728,422
: PRIOR FILING DATE: 2000-11-30
: PRIOR APPLICATION NUMBER: 09/693,325
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 09/663,561
: PRIOR FILING DATE: 2000-09-15
: PRIOR APPLICATION NUMBER: 09/654,936
: PRIOR FILING DATE: 2000-09-01
: PRIOR APPLICATION NUMBER: 09/620,325
: PRIOR FILING DATE: 2000-07-19
: PRIOR APPLICATION NUMBER: 09/598,075
: PRIOR FILING DATE: 2000-06-20
: PRIOR APPLICATION NUMBER: 09/560,875
: PRIOR FILING DATE: 2000-04-27
: PRIOR APPLICATION NUMBER: 09/496,914
: PRIOR FILING DATE: 2000-02-03
: NUMBER OF SEQ ID NOS: 3960
: SOFTWARE: Custom
: SEQ ID NO: 2841
: LENGTH: 374
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-293-244-2841

Query Match      24.7%; Score 157.8; DB 6; Length 374;
Best Local Similarity 70.7%; Pred. No. 8e-30;
Matches 210; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY      206  ATTCGCGACGACGACCCCGACGAAATCCCGGTGATCATGAGCGCTACAGGGTGAGAG 265
DB      6      ATCCGGGTAAGATTCCCAACAATAATCCCGGTGATGAGCGCTACCCAGGAGACG 65
QY      266  CAGCTGCCCTCTCTGGACAAAGCAAGTTTGTGTCCTCCGGACCATGTACATGAGCGAG 325
DB      66      TTCCTGCCCCCGGTGGACAAACCAAGTTCCTGGTCCCGGAGAGCTTACCATGACCCAG 125
QY      326  TTGGTCAAGATCATTCGGCGCGCGCTGAGCTGAACCCACAGAGCCTTCTTCTGCTG 385
DB      126  TTCTGCACATCATTCGGAGCGCGCATGCTCTGGAAGGACGAGGAGCCTTTACTTGCTG 185
QY      386  GTGAACACGACACAGCATGTGATGTGTTCACAGCGCCATCGCGGACATTAAGAGCAGAG 445
DB      186  GTGAACAACAAAGAGCTGTGTGACGATGAGCGCAACCATGCGCAGAGATTTACAGAGACTAC 245
QY      446  AAAGACGAGCAGCGGCTTCTCTATATGTGCTTAAGCGCTCCCAAGAAACCTTGCGCTC 502
DB      246  AAGGATGAGATGAGCTTCTGTACATGACTTAAGCGCTCCAGAGAGACATTTGCGTGC 302

RESULT 8
US-09-654-936A-107
: Sequence 107, Application US/09654936A
: GENERAL INFORMATION:
: APPLICANT: Tang, Y. Tom
: APPLICANT: Liu, Chenghua
: APPLICANT: Asundi, Vinod
: APPLICANT: Zhou, Ping
: APPLICANT: Zhang, Jie
: APPLICANT: Ren, Feiyan
: APPLICANT: Zhao, Qing A.
: APPLICANT: Xue, Aidong J.
: APPLICANT: Wehrman, Tom
: APPLICANT: Wang, Jian-Rui
: APPLICANT: Drmanac, Radoje T.
: TITLE OF INVENTION: Novel Nucleic Acids and
: TITLE OF INVENTION: Polypeptides

```

```
FILE REFERENCE: 787C1P2C
CURRENT APPLICATION NUMBER: US/09/654,936A
CURRENT FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 164
SOFTWARE: PL_FL_genes Version 1.0
SEQ ID NO: 107
LENGTH: 603
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (120)..(527)
US-09-654-936A:107
```

```
Query Match      21.7% Score 138.6; DB 5; Length 603;
Best Local Similarity 66.7%; Pred. No. 5e-25;
Matches 198; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
```

```
QY 140 ATGCCCTCAGACCGGCTTTCAAGCAGCGCGGAGCTTCGCCGACCGCTGTAGAGAGTA 199
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 138 ATCCCAAGCGTCAAGACCTTCAAGCAGAGGAAACCTTGGCAATCAGACAAAGAGAGTT 197
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 200 CAGCAGATCCGCGACGACGACCGCCAGCAAAATCCCGGTATCATCGACCGCTACAAAGGT 259
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 198 GCTGGAATCCGGCGCAAGTTGCCCAACAAATCCCGGTGTAGTGGAGGCGTACACCCAGG 257
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 240 GAGAACGACGCTGCCCTCTCTGACCAAGCAAGTTTGGTCCCGGACCATGTCAACATG 319
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 258 GAGACGTTCTCTGCCCGCTGGACAAACCAAGTTCTGTGTCGCCGAGAGCTGACCAAG 317
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 320 AGCGAGTTGGTCAATATATCGCGCGCGCCCTGTCAGCTGSAACCCAGCAGGCTTTCTTC 379
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 318 ACCCAGTTCTCTAGATATATCGCGAGCGCGCATGCTGTAGAGCCAGCCGAAACCTTTTAC 377
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 380 CTGCTGGTGAACGACGACGACGATGTGTGTCCAGCGCATGCAATGCAATCTAG 436
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 378 TTGCTGTGAACACGACGACGCTGTGTGTCAGCATGACCGCAACGATGCAAGATCTAC 434
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
RESULT 9
US-10-293-244-873
Sequence 873, Application US/10293244
GENERAL INFORMATION:
APPLICANT: Hysq, Inc.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-029
CURRENT APPLICATION NUMBER: US/10/293,244
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: Not Yet Assigned
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 09/728,422
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 09/693,325
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/663,561
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/654,936
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/620,325
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/598,075
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 3960
SOFTWARE: Custom
```

```
SEQ ID NO 873
LENGTH: 603
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (120)..(527)
US-10-293-244-873
```

```
Query Match      21.7% Score 148.6; DB 6; Length 603;
Best Local Similarity 66.7%; Pred. No. 5e-25;
Matches 198; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
```

```
QY 140 ATGCCCTCAGACCGGCTTTCAAGCAGCGCGGAGCTTCGCCGACCGCTGTAGAGAGTA 199
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 138 ATCCCAAGCGTCAAGACCTTCAAGCAGAGGAAACCTTGGCAATCAGACAAAGAGAGTT 197
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 200 CAGCAGATCCGCGACGACGACCGCCAGCAAAATCCCGGTATCATCGACCGCTACAAAGGT 259
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 198 GCTGGAATCCGGCGCAAGTTGCCCAACAAATCCCGGTGTAGTGGAGGCGTACACCCAGG 257
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 260 GAGAACGACGCTGCCCTCTCTGACCAAGCAAGTTTGGTCCCGGACCATGTCAACATG 319
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 258 GAGACGTTCTCTGCCCGCTGGACAAACCAAGTTCTGTGTCGCCGAGAGCTGACCAAG 317
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 320 AGCGAGTTGGTCAATATATCGCGCGCGCCCTGTCAGCTGSAACCCAGCAGGCTTTCTTC 379
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 318 ACCCAGTTCTCTAGATATATCGCGAGCGCGCATGCTGTAGAGCCAGCCGAAACCTTTTAC 377
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 380 CTGCTGGTGAACGACGACGACGATGTGTGTCCAGCGCATGCAATGCAATCTAG 436
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 378 TTGCTGTGAACACGACGACGCTGTGTGTCAGCATGACCGCAACGATGCAAGATCTAC 434
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
RESULT 10
US-09-820-649-94
Sequence 94, Application US/09820649
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 84 Human Secreted Proteins
FILE REFERENCE: P2012P1
CURRENT APPLICATION NUMBER: US/09/820,649
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US/09/246,557
PRIOR FILING DATE: 1999-01-26
PRIOR APPLICATION NUMBER: P01/05386/15949
PRIOR FILING DATE: 1998-07-29
PRIOR APPLICATION NUMBER: 60/054,212
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,209
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,234
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,218
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,214
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,236
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,215
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,211
PRIOR FILING DATE: 1997-07-30
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 353
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 94
LENGTH: 535
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (529)
```

OTHER INFORMATION: n equals a,t,g, or c
US-09-820-649-94

Query Match 15.6%; Score 99.6; DB 5; Length 535;
Best Local Similarity 97.1%; Pred. No. 2e-15;
Matches 99: Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 539 GGGGCCCCGGTACGAGCCCTGCCCCAGAGAGCTTGTGTTCTGTAACCTGAGCTGCTTACC 598
DB 60 SGRGCCCGGCTGAGCGCCCTGCCCCAGAGAGCTGCTGTTCTGTAACCTGAGCTGCTTACC 119
QY 599 GTGGTGGGCTGGGAGGAGATGCCCCCTTACTAGAGGCA 640
DB 120 GTGGTGGGCTGGGAGGAGATGCCCCCTTACTAGAGGCA 161

RESULT 11
US-10-626-717-7205
Sequence 7205, Application US/10626717

GENERAL INFORMATION:
APPLICANT: Andersen, Scott E.
APPLICANT: Byrum, Joseph R.
APPLICANT: De La Pena, Robert C.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS
FILE REFERENCE: 38-21(15878)D
CURRENT APPLICATION NUMBER: US/10/626,717
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US 10/304,123
PRIOR FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: US 09/594,596
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 10952
SEQ ID NO 7205
LENGTH: 448
TYPE: DNA
ORGANISM: Triticum aestivum
FEATURE:
OTHER INFORMATION: Clone ID: uc-tsrow189015e11b1
US-10-626-717-7205

Query Match 11.0%; Score 70.4; DB 6; Length 448;
Best Local Similarity 54.8%; Pred. No. 2.9e-08;
Matches 184: Conservative 0; Mismatches 146; Indels 6; Gaps 2;

QY 156 CTTTCAGACAGCGGGGAGCTTCGCGGACCGCTGTAGAGAGGTACAGAGATCCCGACC 215
DB 119 CGTTCAAGCTGGAGCAGCCGCTCGAGAGAGGAGGAGGAGGCTTAACGCAATAGAGAGA 178
QY 216 AGCACCAGCAAAATCCCGGTGATCATCGAGCGCTACAGAGGAGTGAAGACAGCTGCCG 275
DB 179 AGTACTGTGACAGAAATTCCTGTGATCGTTGAG--AAAGCTGGGAGAGGTGATATCTCTG 235
QY 276 TCTGAGACAGCAAGTTTGTGTCGCGGACCATGTCAACATGAGCGAGTGGTCAAGA 335
DB 236 ACATTGACAAGAAAGATACCTGCTCCCGGACCTTAAGTGTGACAGTTCGTTATG 295
QY 336 TCATCCGGCGGCGCTGCAAGCTGAAGCCAGCAGGCGCTTCTCTGCTGTGTAACCAAC 395
DB 296 TTGTCGGAGAGCGGATCAAGCTCAAGTGTGAAGAGGAGCATCTTATCTTTGTA--AGA 352
QY 396 ACAGCATGTGATGTGTCACGCCATCGCGGACATCTAGACAGAGAGAGAGAGAGAG 455
DB 353 ACATCTTCCACAGCAGAGCTGCGCTGATGTGTCATTTAGAGAGAGAGAGAGAGAGAG 412
QY 456 ACAGCTCTCTATATGTTAGTACGCGCTCCAGAGAA 491
DB 413 ACAGCTCTCTATATGTTAGTACGCGCTCCAGAGAA 448

RESULT 12
US-10-085-783A-26616
Sequence 26616, Application US/10085783A

GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.

APPLICANT: Liew, C.C.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

FILE REFERENCE: 4231/2002

CURRENT APPLICATION NUMBER: US/10/085,783A

CURRENT FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR FILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: PatentIn version 3.2

SEQ ID NO 26616

LENGTH: 469

TYPE: DNA

ORGANISM: Human

US-10-085-783A-26616

Query Match 9.9%; Score 63.6; DB 6; Length 469;
Best Local Similarity 50.7%; Pred. No. 1.4e-06;
Matches 206: Conservative 0; Mismatches 194; Indels 6; Gaps 2;

QY 101 CCCAGAGCCCGGCTGCGCGCCAGCCGCGCCGCGCATGCTTCAAGACCGGCTTTC 160
DB 35 CTCGGCGGCTCGCGGAGCGCGGCTTCCCTTCCCGCGCCGCGCATGAGTGGATGTC 94
QY 161 AAGCAGCGCGGAGGCTTCCGCGCGCGCTGTAGAGAGTACAGAGATCCGCGAGCAGC 220
DB 95 AAGGAGAGCAGCTCCGCTGAGACAGAGATGCGGAGTCCGCGAGATTCGAGCAAAAT 154
QY 221 CCCAGCAAAATCCCGGTATCATGAGCGCTCAAGAGGTGAGAGAGAGAGAGAGAG 280
DB 155 CCCGACAGGCTTCCGCTGATGTGTGAAGAGTCTAGG--CTTCAAGTGTTCATAT 211
QY 281 GACAAAGACCAAGTTTGTGTCGCGGAGCAGTGTCAACATGAGGAGTGTGTCAGATCAT 340
DB 212 GACAAAGAGAGTACTGTTGTTCTCATCTGATCATCTGATGATGATGATGATGAT 271
QY 341 CGGCGCGGCTGAGCTGAGTACAGCCGAGCGGCTTCTGCTGCTGATGAGCAGCAGC 400
DB 272 AGGAAAGAGATCCAGCTTCTTGTGAAGAGGAGATCTTCTTGTGATTAAGACAGTC 331
QY 401 ATGTGATGTGTGTCAGCGCCATCCGAGCATCTACGAGAGAGAGAGAGAGAGAGAG 460
DB 332 CCACAGTCCAGCTTACT--ATGGAGACGCTTTACGAGAGAGAGAGAGAGATGAGATG 388
QY 461 TTCTCTATATGTTAGTACGCGCTCCAGAGAAACCTTGGCTTCTGAG 506
DB 389 TTCTATATGTGGCTTACAGCGGAGAGAGAACTTTGGCTTCTGAG 434

RESULT 13
US-10-085-783A-10191
Sequence 10191, Application US/10085783A
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10191

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? LENGTH: 400
? TYPE: DNA
? ORGANISM: Human
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (17)..(17)
? OTHER INFORMATION: n is a, c, q, or t
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (35)..(35)
? OTHER INFORMATION: n is a, c, q, or t
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (37)..(37)
? OTHER INFORMATION: n is a, c, q, or t
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (382)..(382)
? OTHER INFORMATION: n is a, c, q, or t
US-10-085-783A.10191
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Query Match 8.9%; Score 57; DB 6; Length 400;
Best Local Similarity 55.2%; Pred. No. 5.7e-05;
Matches 133; Conservative 0; Mismatches 105; Indels 3; Gaps 1;

```
QY 266 CAGCTGGCCGCTCTGACAAAGACCAAGTTTGTGTCGGGACACATGTCAGATGAGCGAG 325
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 117 CAGATTGTGTCAGATGACAAAGGAGAGTACTGTGTCATGATGATGATGATGATGATGATG 176

QY 326 TTGCTCAAGATCATCGGCGCGCGCTCGAGCTGAACCCGACGAGCGCTTCTCTGCTG 385
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 177 TTGATGTGATCATCAGCAAAAGGATCCAGCTTCTCTGTGAAGAGGATCTTCTCTGTTT 236

QY 386 GTGACGACGACACACATGCTGATGCTGCTCCAGCGCCATCGCGGACATCTAGCAGAGAG 445
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 237 GTGATATGACAGCTGCCACAG---TCCAGCCTAACTATGAGGACGAGCTTACGAGAAAGAA 293

QY 446 AAAAGCAGGAGGAGCGCTTCTCTATATGCTCTAGCGCTCCGAGAAACCTTGCGCTTCTGA 505
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 294 AAAGATGAGAGATGATTTCTTATATGCTGCGCTACAGGAGGAGAGAACATTTTGGCTTCTGA 353

QY 506 G 506
Db 354 G 354
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RESULT 14

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US-10-085-783A-20079
? Sequence 20079, Application US/10085783A
? GENERAL INFORMATION:
? APPLICANT: ChondroGene Inc.
? APPLICANT: Liew, C.C.
? TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
? FILE REFERENCE: 4231/2002
? CURRENT APPLICATION NUMBER: US/10/085,783A
? PRIOR FILING DATE: 2002-02-28
? PRIOR APPLICATION NUMBER: US 60/305,340
? PRIOR FILING DATE: 2001-07-13
? PRIOR APPLICATION NUMBER: US 60/275,017
? PRIOR FILING DATE: 2001-03-12
? PRIOR APPLICATION NUMBER: US 60/271,955
? PRIOR FILING DATE: 2001-02-28
? NUMBER OF SEQ ID NOS: 58994
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 20079
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? LENGTH: 194
? TYPE: DNA
? ORGANISM: Human
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (18)..(18)
? OTHER INFORMATION: n is a, c, q, or t
? FEATURE:
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? NAME/KEY: misc_feature
? LOCATION: (24)..(24)
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? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (165)..(165)
? OTHER INFORMATION: n is a, c, q, or t
US-10-085-783A-20079
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Query Match 8.8%; Score 56.6; DB 6; Length 194;
Best Local Similarity 75.2%; Pred. No. 5.7e-05;
Matches 82; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

```
QY 388 GAACGACGACAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 446
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 GAACGGGTACAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60

QY 447 AAGACGAGGAGCGGCTTCTCTATATGATGATGATGATGATGATGATGATGATGATGAT 495
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AAGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 109
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RESULT 15

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US-10-085-783A-52126
? Sequence 52126, Application US/10085783A
? GENERAL INFORMATION:
? APPLICANT: ChondroGene Inc.
? APPLICANT: Liew, C.C.
? TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
? FILE REFERENCE: 4231/2002
? CURRENT APPLICATION NUMBER: US/10/085,783A
? PRIOR FILING DATE: 2002-02-28
? PRIOR APPLICATION NUMBER: US 60/405,340
? PRIOR FILING DATE: 2001-07-13
? PRIOR APPLICATION NUMBER: US 60/275,017
? PRIOR FILING DATE: 2001-03-12
? PRIOR APPLICATION NUMBER: US 60/271,955
? PRIOR FILING DATE: 2001-02-28
? NUMBER OF SEQ ID NOS: 58994
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 52126
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? LENGTH: 380
? TYPE: DNA
? ORGANISM: Human
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (31)..(31)
? OTHER INFORMATION: n is a, c, q, or t
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (57)..(57)
? OTHER INFORMATION: n is a, c, q, or t
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? NAME/KEY: misc_feature
? LOCATION: (289)..(289)
? OTHER INFORMATION: n is a, c, q, or t
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (346)..(346)
? OTHER INFORMATION: n is a, c, q, or t
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: (368)..(368)
? OTHER INFORMATION: n is a, c, q, or t
US-10-085-783A-52126
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Query Match 8.4%; Score 54; DB 6; Length 380;
Best Local Similarity 54.7%; Pred. No. 0.00031;
Matches 127; Conservative 0; Mismatches 102; Indels 3; Gaps 1;

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    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 14 GTCATTGACAAAGCAAGATTTTGTGTCGGGACATGTCAGATGAGGAGATTTGGATTAAG 74
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OM nucleic - nucleic search, using sw model

Run on: August 15, 2003, 07:57:30 : Search time 2040 seconds
(without alignments)
7624.934 Million cell updates/sec

Title: US-09-904-603-2
Perfect score: 640
Sequence: 1 CTCGCCGACGCCGACGCCGCGCC.....GCCCCCTAGTCAGAGGCGCA 640

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: em_estba:*
2: em_esthum:*
3: em_estlin:*
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5: em_estlin:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	627.4	98.0	1149	BM925959 AGNCOURT
2	625.8	97.8	1074	BM919877 AGNCOURT
3	598.8	93.6	700	BM67032 603291206
4	593.4	92.7	10	BM715828 602675240

5	590.4	92.2	1094	BM919896
6	584.4	91.3	1115	BM924606
7	583.6	91.2	794	BM1601673
8	582.4	91.0	738	BM824755
9	575.8	90.0	1151	BM924607
10	573.6	89.6	730	BM1522709
11	563.4	88.0	676	BM1918612
12	560	87.5	594	BE885329
13	534	83.4	1281	BM067721
14	514.4	80.4	560	BM111122
15	513	80.2	561	BM166829
16	501	78.3	766	BM708209
17	488	76.2	514	BM151709
18	485.2	75.8	528	BM712961
19	483.8	75.6	1009	BM723424
20	482.6	75.4	614	BM450406
21	474.4	74.1	500	BM163154
22	474.4	74.1	546	BM784127
23	464	72.5	476	BM161293
24	447.8	70.0	623	BM826481
25	436.2	68.2	894	BM321417
26	433.4	67.7	633	BM962192
27	432.8	67.6	595	BM946584
28	428.4	66.9	513	BM115760
29	425.2	66.4	953	BM4003716
30	424.4	66.3	655	BM444944
31	422.4	66.0	961	BM050653
32	417.4	65.2	555	BM613461
33	417	65.2	501	BM383216
34	416.4	65.1	864	BM1735232
35	415.2	64.9	688	BM383578
36	414.4	64.8	543	BM881349
37	413.2	64.6	963	BM4015020
38	413.2	64.6	965	BM703975
39	409.4	64.0	680	BM322683
40	409.2	63.9	1065	BM300927
41	406.4	63.5	866	BM604726
42	406.4	63.5	954	BM4003122
43	405.4	63.3	977	BM703479
44	402	62.8	418	BM712843
45	401.4	62.7	441	BM712850

ALIGNMENTS

RESULT 1
LOCUS
DEFINITION BM925959 1149 bp mRNA linear EST 12-MAR-2002
AGNCOURT_5649827 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5754355
5' UTR mRNA sequence.
ACCESSION BM925959
VERSION BM925959.1 GI:19376434
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;
1 (bases 1 to 1149)
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNC)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNC at:
<http://image.llnl.gov>
Plate: L1AM12817 row: m column: 04
High quality sequence start: 3

Position	Sequence	Position	Sequence
Db	ACCCACGACGAGCCTTCTTCTCGTGGTGAACACACAGCA TGTGTGAGTGTGTTCACGC	434	
Qy	CCATTCGCGACATCTACGACGAGGAAAAGACGAGACGGCTTCTCTATATGTGTCTACG	479	
Lb	CCATGCGCGACATCTACGACGAGGAAAAGACGAGACGGCTTCTCTATATGTGTCTACG	494	
Qy	CCTCCGACGAAACCTTGCGCTTCTTGAGCGACAGTAGGGGGGCGTGGGCGCTGGAGCTCGGG	539	
Lb	CCTCCGACGAAACCTTGCGCTTCTTGAGCGACAGTAGGGGGGCGTGGGCGCTGGAGCTCGGG	554	
Qy	GGGCGCGCGGTAGGCGCTTGCCACGAGACCTTGTGTTCTAACTAGAGCTGGCTCTACGG	599	
Lb	CGCGCGCGGTAGGCGCTTGCCACGAGACCTTGTGTTCTGTAACCTGAGCTGGCTCTACGG	614	
Qy	TGCTGTGGCTGGGACGAGCATGTGCCCTCTAGTCAGAGGCA	640	
Lb	TGCTGTGGCTGGGACGAGCATGTGCCCTCTAGTCAGAGGCA	655	

RESULT 3	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE
R1667032	603291206P1	700 bp mRNA	R1667032	R1667032	EST	Homo sapiens (human)
	MIH_MGC_96	linear		GI:15581265		
		cdna clone				
		IMAGE:53108405				

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 700)		National Institutes of Health, Mammalian Gene Collection (MGC)		
		Unpublished		
		Contact: Robert Strausberg, Ph.D.		

Contact: Robert Strassberg, Ph.D.
Email: c9abbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D. (NHGRI), Shirakawa
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Preparation: Michael J. Brownstein (NHGRI)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM11787 row: k column: 01
High quality sequence stop: 694.

FEATURES	Location/Qualifiers
source	1. .700

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5310840"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/clone_id="N1H_MGC_96"
/notes="Organ: brain; Vector: pBluescript (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dt primed using primer 5'-tttttttttttttttVN-3',
size-selected for average insert size 2.3 kb and
normalized to R0T 5. This is a primary library enriched
for full-length clones and constructed using the
CAP-trapper method (Carriacci, in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a N1H_MGC Library."

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Query Match:	93.6%	Score 598.8:	DB 12:	Length 700:
Best Local Similarity:	98.1%:	Pred. No. 5.1e-114:		
Matches 506:	Conservative	0:	Mismatches 12:	Indels 0:
				Gaps 0:

[illegible][illegible]

RESULT 4
BG715828

LOCUS	705 bp	mRNA	linear	EST 08-MAY-200
DEFINITION	602675240F1	NIH-MGC_96 Homo sapiens	CDNA clone IMACH:477944_5'	
mRNA sequence.				

ACCESSION	BC715828
VERSION	BC715828.1
KEYWORDS	GI:13995015 EST.

SOURCE	ORGANISM
Homo sapiens (human)	Homo sapiens
Ensembl	Eumetazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo: 1 (bases 1 to 705)
NCBI-MG	http://ncicci.nih.gov/
National Institutes of Health	National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished	Contact: Robert Strassberg, Ph.D.

Tissue Procurement: Mikiros Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHRI), Shitaki
Toshiyuki and Piero Carninci (IKBEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI at:
<http://image.jnl.gov>
Plate: L1AM10684 row: P column: 10
High quality sequence stop: 697.

db	QY	Db	QY	Db	QY	Db	QY	Db	QY	Db	
361	CAGCATGAGTGTGTGCACGCCCATCGCGGACATCTACGAGCAGAGGAAGAAGCAGAGA	420	457	CGGCTTCCTATATATGCTCTACGGCTCCGACGAAACCTTGCGTTCTATAGCAGAGTAG	516	421	CGGCTTCCTATATATGCTCTACGGCTCCGACGAAACCTTGCGTTCTATAGCAGAGTAG	480	517	GGGGGCTTCGAGCTTGAGGAGTGGGGGGCCCTCGGTCTAGGCTCTGCCAGAGACTTGTGTT	576
481	GGGGGCTTCGAGGATCGGGGGGGCCCGGTCTAGGCTCTGCCAGAGACTTGTGTT	540	577	CCTGAAGCTGAGCTCCTCTTACCGTGGTGGGCTGGGACAGGCATGTGCCCCCTAGTCAGAG	636	541	CCTGAAGCTGAGCTCCTCTTACCGTGGTGGGCTGGGACAGGCATGTGCCCCCTAGTCAGAG	600	637	GGCA	640
601	GGCA	604	601	GGCA	604						

RESULT	6
BM924606	
LOCUS	1115 bp
DEFINITION	mRNA linear EST 12-MAR-2002
	ACNCCOURT_6767666 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:57609940

ACCESSION	BM924606
VERSION	BM924606.1 GI:19374985

SOURCE Homo sapiens (human)

REFERENCE	(bases 1 to 1115)
AUTHORS	NIH-MGC http://mgc.ncbi.nlm.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D.

Email: c9abbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM12808 row: o column: 07
 High quality sequence set: 573.

FEATURES	Location/Qualifiers
source	1., 115

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5760950"
/lab_host="DH10B"
/clone_1b="NH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (ecoRV site is
destroyed upon cloning). Average insert size 1.4 Kb,
insert size range 1-3 Kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NH_MGC library."
BASE COUNT      125 a      375 c      389 g      114 t      112 others

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Query Match	91.3%	Score 584.4	DB 12	Length 115
Best Local Similarity	99.5%	Pred. No. 5.2e-111		
Matches 597	Conservative	0	Mismatches 1	Indels 2
				Gaps 1

QY	43	CCCTTAGCGCGCAGAGGCGCGCAAGCGCC--GGAGCGCGCGCAACCGCGAGATATGCGCGCG	140	
Pb	1	CCCTTAGCGCGCAGAGGCGCGCAAGCGCCCGCAGCGAGCGCGCAACCGCGAGATATGCGCGCGCG	140	
QY		101	CCGAGAGCGCGCGCGCTTCGCGCGCGCGAGCGCGCGCGCGCGGATCGCTTAAAGCGCGCGTTTC	146
Pb	61	CCGAGAGCGCGCGCGCGCTTCGCGCGCGCGAGCGCGCGCGCGCGGATCGCTTAAAGCGCGCGTTTC	146	
QY	161	AAGTAAGCGCGAGGTTTCGCGCGAGCGCGCTTAAAGCGCGCGTAAAGCGAGATCGCGAGATCGTAG	220	
Pb	121	AAGGAGGCGCGAGGTTTCGCGCGAGCGCGTAAAGCGAGTAAAGCGAGATCGCGAGCGTAG	180	
QY	221	CCGAGCGAAATCCCGGTGATTCATCGAGCGCGTAAAGGTTGAGAGCGATTCGCGCGCGCGCG	286	
Pb	181	CCGAGCGAAATCCCGGTGATTCATCGAGCGCGTAAAGGTTGAGAGCGATTCGCGCGCGCGCG	246	
QY	281	GACAGAGCCCAAGTTTTCGTCGCGGAGGATATGCAACATGAGCGAGTTGATTAAGATATATC	440	
Pb	241	GACAGAGCCCAAGTTTTCGTCGCGGAGGATATGCAACATGAGCGAGTTTGTATTAAGATATATC	400	
QY	341	CGCGCGCGCGTCAAGTGAAGCGCGATGAGCGCGTTTCGTCGCGTGAATATATGATATATC	400	

[illegible]

RESULT 7	LOCUS	DEFINITION	ACCESSION
B1601673	603249142P1	794 bp mRNA 603249142P1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:5301554 5', mRNA sequence.	B1601673 B1601673.1 GI:15494612

SOURCE ORGANISM	Homo sapiens (human)
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REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Carnivora: Homnidae: Homo.
AUTHORS	1 (bases 1 to 794)
TITLE	NIH-MGC http://mgi.cni.nih.gov/ .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished
	Contact: Robert Strausberg, Ph.D.

Email: ccapsd-remail@ihh.gov
Tissue Procurement: Mikiros Palokivits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NETR), Shitaki
Toshiyuki and Piero Carninci (PIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (IHLN)
DNA Sequencing by: Invitae Genomics, Inc.
Clone distribution: MOC clone distribution information can be
found through the I.M.A.G.E. Consortium/IHLN at:
<http://image.ihl.gov>
Plate: LLAM1763 row: h column: 93
High quality sequence stop: 751.

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FEATURES      Location/Qualifiers
source        1..794
              /organism="Homo sapiens"
              /mol_type="mRNA"
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/db_xref="taxon:9606"
 /clone="IMAGE:530154"
 /issue_type="hypochalampus"
 /lab_host="DH10B"
 /clone.lib="NIH_MGC_96"
 /note="Organ: brain; Vector: pBluescript (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dt primed using primer 5'-TTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC library."

BASE COUNT 138 a 264 c 250 g 142 t

ORIGIN

Query Match 91.2%; Score 583.6; DB 12; Length 794;
 Best Local Similarity 99.0%; Pred. No. 7.2e-111;
 Matches 608; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

28 GCGCGAGCCCGGAGCCCTTGTAGCGGAGCGCGAG-CCCGGAGCCCAACCGCAG 86
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 4 GGGCTAGCCCGGAGCCCTTGTAGCGGAGCGCGAGCGCGAGCCCGGAGCCCAACCGCAG 63
 87 ACACATCCCGGCGCCGAGCGCCGCGCTGGCGCCCAAGCGGCGCGCGGATGCCCT 146
 1
 64 ACACATCCCGGCGCCGAGCGCCGCGCTGGCGCCCAAGCGGCGCGGATGCCCT 123
 147 CAGACCGGCGCTTCAAGCAGCGGCGGAGCTTGGCGAGCGGCTTAAGGAGTACAGCA 206
 1
 124 CAGACCGGCGCTTCAAGCAGCGGCGGAGCTTGGCGAGCGGCTTGAAGGAGTACAGCA 183
 207 TCCGCGAGCAGCAGCCCAAGCAAAATCCGGTATCATCAGCGCTACAGAGGTGAGAAC 266
 184 TCCGCGAGCAGCAGCCCAAGCAAAATCCGGTATCATCAGCGCTACAGAGGTGAGAAC 243
 267 AGCTCCCGCTCTGACAAAGAACAGTTTGTGTCGCCGAGCATGTCAATGAGCAGCT 326
 1
 244 AGCTCCCGCTCTGACAAAGAACAGTTTGTGTCGCCGAGCATGTCAATGAGCAGCT 303
 327 TGGTCAAGATCATCCGCGCGCGCTGACAGCTGACAGCCCAAGCGGCTTCTGCGTGG 386
 1
 304 TGGTCAAGATCATCCGCGCGCGCTGACAGCTGACAGCCCAAGCGGCTTCTGCGTGG 362
 387 TGAACCCAGCAGCATGTGTGTCACAGCCCATGCGGAGCATCTACAGCAGAGAGA 446
 363 TGAACCCAGCAGCATGTGTGTCACAGCCCATGCGGAGCATCTACAGCAGAGAGA 422
 447 AAGACGAGGAGCGCTTCTGATATGATGCTACGCTCCAGAAACCTTGGCTTCTGAG 506
 1
 423 AAGACGAGGAGCGCTTCTGATATGATGCTACGCTCCAGAAACCTTGGCTTCTGAG 482
 507 CCAGCAGTAGGGGGGCTGCGGCTGCGGAGTCCGGGGGCGCGCTACGCGCTCCAGAGA 566
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 483 CCAGCAGTAGGGGGGCTGCGGCTGCGGAGTCCGGGGGCGCGCTACGCGCTCCAGAGA 542
 567 GCTTGTGCTTCTGACTGAGTGCCTTACCGGTGCGGCTGCGGAGGAGCATGTCCGCC 626
 1
 543 GCTTGTGCTTCTGACTGAGTGCCTTACCGGTGCGGCTGCGGAGGAGCATGTCCGCC 602
 627 CTAGTCAGAGGGA 640
 1
 603 CTAGTCAGAGGGA 616

RESULT 8
 B1824755 738 bp mRNA linear EST 04-OCT-2001
 LOCUS 6030336361 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5174817 5',
 DEFINITION mRNA sequence.
 ACCESSION B1824755
 VERSION B1824755.1 GI:15936305

KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 738)
 NIH-MGC <http://mhc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cygphs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA library preparation: Life Technologies, Inc.
 DNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLM11435 row: 9 column: 10
 High quality sequence stop: 718.
 Location/Qualifiers

FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5174817"
 /lab_host="DH10B"
 /clone.lib="NIH_MGC_115"
 /note="Organ: pooled brain, lung, testis; Vector: PCMV-SPORE; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dt primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb; library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research genetics tracking code 021. Note: this is a NIH_MGC Library."

BASE COUNT 132 a 244 c 236 g 126 t

ORIGIN

Query Match 91.0%; Score 582.4; DB 12; Length 738;
 Best Local Similarity 99.7%; Pred. No. 1.3e-110;
 Matches 594; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

46 TTGACCGGAGCGCGGAG-CCCGGAGCCCAACCGCAGCATCCCGGCCCA 104
 1
 1 TTGACCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 60
 105 GAGCCCGGCGCTGCGCGCCCAAGCGCGGCGCGGAGCGCGGAGCGCGGCGCTTCAAGC 164
 1
 61 GAGCCCGGCGCTGCGCGCCCAAGCGCGGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 120
 165 AGCGCGGAGCGCTTGGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 224
 1
 121 AGCGCGGAGCGCTTGGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGG 180
 225 GCAAAATCCCGGTATCATCGAGCGCTTCAAGAGGTGAGAAGAGAGAGAGAGAGAGAGAGAGAG 284
 1
 181 GCAAAATCCCGGTATCATCGAGCGCTTCAAGAGGTGAGAAGAGAGAGAGAGAGAGAGAGAGAG 240
 285 AGACCAAGTTTGTGCTCCCGGAGCATGTCACATGAGGAGGAGTGGTCAAGATCATCGGCG 344
 1
 241 AGACCAAGTTTGTGCTCCCGGAGCATGTCACATGAGGAGGAGTGGTCAAGATCATCGGCG 300
 345 GCGCGTGCAGCTGAGACCCCAAGCGGAGCGGCTTCTCTGCTGTGAGACGACAGCATGAG 404
 1
 301 GCGCGTGCAGCTGAGACCCCAAGCGGAGCGGCTTCTCTGCTGTGAGACGACAGCATGAG 360
 405 TGAGTGTTCACGCGCATTCGCGAGCATCTACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 464
 1
 361 TGAGTGTTCACGCGCATTCGCGAGCATCTACAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

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OY 465 TCATATGCTCTACGCTCCCGAGAACTTCGCTCTCTGAGCCAGAGTAGAGGGGGCTC 524
      |||||||
Db 421 TCATATGCTCTACGCTCCCGAGAACTTCGCTCTCTGAGCCAGAGTAGAGGGGGCTC 480
OY 525 GGCTTGAGAGTCGGGGGGCCCGGTGACAGCCCTGCCAGAGAGCTTGTGTTCTGAAC 584
      |||||||
Db 481 GGCTTGAGAGTCGGGGGGCCCGGTGACAGCCCTGCCAGAGAGCTTGTGTTCTGAAC 540
OY 585 GAGCTGCTCTACGCTGGTGGGCGGAGGCATGTGCTCCCTAGTCAGAGGGGCA 640
      |||||||
Db 541 GAGCTGCTCTACGCTGGTGGGCGGAGGCATGTGCTCCCTAGTCAGAGGGGCA 596

RESULT 9
HM924607 1151 bp mRNA Linear EST 12-MAR-2002
LOCUS 5', mRNA sequence.
DEFINITION BM924607
ACCESSION BM924607
VERSION BM924607.1 GI:15374986
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1151)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: rgs@biml.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12808 row: c column: 08
High quality sequence start: 44
High quality sequence stop: 718.
Location/Qualifiers
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/clone="IMAGE:5760991"
/lab_host="DH10B"
/clone_lib="NIH_MGC_116"
/note="Organ: pooled colon, kidney, stomach; Vector:
PCMV-SPO8T6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 25 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dt primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
BASE COUNT 190 a 317 c 409 g 196 t 39 others
ORIGIN
Query Match 90.0%; Score 575.8; DB 12; Length 1151;
Best Local Similarity 99.8%; Pred. No. 3,1e-109;
Matches 575; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 65 CCGCGAGCCCGCAACCGCAGACATCCCGCGCCGAGAGCCCGCTCGCGGCC 124
      |||||||
Db 54 CCGCGAGCCCGCAACCGCAGACATCCCGCGCCGAGAGCCCGCTCGCGGCC 113
OY 125 AGCGGCGCGCGCGGATGCGCTCAGACCGGCGCTTCAAGCAGCGCGCTTGGCGGAC 184
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Db 114 AGCGGCGCGCGCGGATGCGCTCAGACCGGCGCTTCAAGCAGCGCGGAGCTTGGCGGAC 174
OY 185 CGCTGTAGAGAGGTACATATCCGTGAGTACAGACCCGACAAATTCGGTATCATC 244
      |||||||
Db 174 CGCTGTAGAGAGGTACATATCCGTGAGTACAGACCCGACAAATTCGGTATCATC 233
OY 245 GAGGCGCTACAGAGGTGAGAACGACGTGCGCGCTCGCGAGAGGACCAAGTCTTCTGCTG 304
      |||||||
Db 234 GAGGCGCTACAGAGGTGAGAACGACGTGCGCGCTCGCGAGAGGACCAAGTCTTCTGCTG 293
OY 305 GAGCATGTCAACATAGAGGAGCTGTGATCATATCCGCGCGCGCTGCTGATCAATGCT 464
      |||||||
Db 294 GAGCATGTCAACATAGAGGAGCTGTGATCATATCCGCGCGCGCTGCTGATCAATGCT 353
OY 365 AGCGAGGCTTCTTCTGCTGTGATATAGACAGCATGTGTGATGTGTGTGAGCGCTATC 424
      |||||||
Db 354 AGCGAGGCTTCTTCTGCTGTGATATAGACAGCATGTGTGATGTGTGTGAGCGCTATC 413
OY 425 GCGGACATCTACGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 484
      |||||||
Db 414 GCGGACATCTACGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 473
OY 485 CAGGAAATCTTCGCTCTGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 544
      |||||||
Db 474 CAGGAAATCTTCGCTCTGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 533
OY 545 CCGGTGAGCGCTGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 604
      |||||||
Db 534 CCGGTGAGCGCTGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 593
OY 605 GCGTGGCGAGCATGTGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 640
      |||||||
Db 594 GCGTGGCGAGCATGTGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 629

RESULT 10
B1522709 730 bp mRNA Linear EST 29-AUG-2001
LOCUS 603175758P1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240007 5'
DEFINITION B1522709
ACCESSION B1522709
VERSION B1522709.1 GI:15347501
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 730)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: rgs@biml.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Lucite Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11605 row: c column: 16
High quality sequence stop: 740.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5240007"
/lab_host="DH10B"
/clone_lib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPO8T6; Site:1: NotI;
Site:2: EcoRV (destroyed); RNA source anonymous pool of
fetal brains, female and 20 weeks, female and 24 weeks."
FEATURES
Source

```

and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH-MGC Library."

BASE COUNT 129 a 245 c 242 g 114 t
ORIGIN

Query Match 89.6%; Score 573.6; DB 12; Length 730;
Best Local Similarity 98.0%; Pred. No. 3e-109;
Matches 623; Conservative 0; Mismatches 9; Indels 4; Gaps 4;

9 GCCGAGCCGCGCTCTAGCGCGAGCCCGGAGCCCTTGGAGCGGAGCGGAGCCCC 68
1 GCCGAGCCGCGCTCTAGCGCGAGCCCGGAGCCCTTGGAGCGGAGCGGAGCCCC 60
69 G-GAGCCCGCAACGGCAGACATCCCGGCGCCCGAGAGCC-CCGGCTTGGCGCCCG 126
61 GCGGAGCCCGCAACGGCAGACATCCCGGCGCCCGAGAGCCCGGCTTGGCGCCCG 120
127 CCGGCGCCCGGCGATGCCCTCAGACCGGCTTTCAGAGCGGCGAGCTTGGCGGACG 186
121 CCGGCGCCCGGCGATGCCCTCAGACCGGCTTTCAGAGCGGCGGAGCTTGGCGGACG 180
187 CTGTAGAGAGTACAGCAGATCCGAGACCGAGCCCAAAATCCGGGTGATCATCA 246
181 CTGTAGAGAGTACAGCAGATCCGAGACCGAGCCCAAAATCCGGGTGATCATCA 240
247 GCGGTACAGAGGTGAGAGCAGCTCCCGCTCTGACAAAGACAGTTTGGTCCCGGA 306
241 GCGGTACAGAGGTGAGAGCAGCTCCCGCTCTGACAAAGACAGTTTGGTCCCGGA 300
307 CCATGTCAACATGAGCGAGTTGGTCAAGATCATCCGCGCGCCGCTTGCAGTGAACCCA 365
301 CCATGTCAACATGAGCGAGTTGGTCAAGATCATCCGCGCGCCGCTTGCAGTGAACCCA 360
366 CGCAGGCTTCTCTCTGCTGTGAACAGCAGACAGCATGAGTGTGTCACGCCATCG 425
361 CGCAGGCTTCTCTCTGCTGTGAACAGCAGACAGCATGAGTGTGTCACGCCATCG 420
426 CGGACATCTAGAGAGAGAGAAAGAGAGAGGCTTCTCT-TATATGCTACGCCCTCC 484
421 CGGACATCTAGAGAGAGAGAAAGAGAGAGGCTTCTCTGTAATATGCTACGCCCTCC 480
485 CAGGAACTTTCGCTTCTGAGCCAGCAGATAGGGGGCTCGGCTGAGAGTGGGGGCC 544
481 CAGGAACTTTCGCTTCTGAGCCAGCAGATAGGGGGCTCGGCTGAGAGTGGGGGCC 540
545 CCGGAGGCGCCCTGCGCAGAGAGTCTGCTTCTGAACTGAGCTGCTTACCGTGTG 604
541 CCGGAGGCGCCCTGCGCAGAGAGTCTGCTTCTGAACTGAGCTGCTTACCGTGTG 600
605 GGCTGGCAGAGATGTGCCCCCTAGTACAGAGGA 640
601 GGCTGGCAGAGATGTGCCCCCTAGTACAGAGGA 636

RESULT 11
LOCUS B1918612 676 bp mRNA linear EST 16-OCT-2001
DEFINITION 60317655F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5241013 5',
mRNA sequence.
ACCESSION B1918612
VERSION B1918612.1 GI:16182288
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 676)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgrahbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNL1607 row: m column: 14
High quality sequence start: 2
High quality sequence stop: 671.
Location/Qualifiers
1. 676
/organism="Homo sapiens"
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/lab_host="DH10B"
/clone.lib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH-MGC Library."

FEATURES
source

BASE COUNT 123 a 223 c 217 g 113 t
ORIGIN

Query Match 88.0%; Score 563.4; DB 12; Length 676;
Best Local Similarity 98.8%; Pred. No. 1.1e-106;
Matches 578; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

56 GCGCGGAGCCCGGAGCCCGCAACCGCAGACATCCCGGCGCCGAGAGCCCGGCC 115
3 GATGTGAGAGCCCGGAGCCCGCAACCGCAGACATCCCGGCGCCGAGAGCCCGGCC 62
116 TCGCGCCGAGCCCGGCGCGATGCCCTTCAAGACCGGCGCGGAGC 175
63 TCGCGCGCAGCCCGGCGCGATGCCCTTCAAGACCGGCGCGGAGC 122
176 TTGCGCGACCGCTGTAAGAGGTACAGCATCCGCGACACACCAAAATCCCG 235
123 TTGCGCGACCGCTGTAAGAGGTACAGCATCCGCGACACCAAAATCCCG 182
236 GTGATCATGAGCGCTTACAGAGGTGAGAGAGTGGCCGCTGAGCAAGCAAGTTT 295
183 GTGATCATGAGCGCTTACAGAGGTGAGAGAGTGGCCGCTGAGCAAGCAAGTTT 242
296 TTGCTCCCGGACCATGTACATGAGCGAGTTGGTCAAGATCATCCGCGCGCTGAG 355
243 TTGCTCCCGGACCATGTACATGAGCGAGTTGGTCAAGATCATCCGCGCGCTGAG 302
356 CTGAACCCGACGAGCGCTTCTTCTGCTGTGTAACAGCAGCATGTGATGTGTC 415
303 CTGAACCCGACGAGCGCTTCTTCTGCTGTGTAACAGCAGCATGTGATGTGTC 362
416 ACGCCCATCGCGGACATCTAGAGAGAGAGAAAGCGAGAGCGGCTTCTTATATGTC 475
363 ACGCCCATCGCGGACATCTAGAGAGAGAGAAAGCGAGAGCGGCTTCTTATATGTC 422
476 TACGCTTCCAGAGAACTTGGCTTGTGAGCCAGCATAGAGGGGCTCGGCTGGAGT 535
423 TACGCTTCCAGAGAACTTGGCTTGTGAGCCAGCACTA-GGGGCTCGGCTGGAGT 481
536 CCGGCGCGCCCGGCTGAGGCTTGGCCAGAGAGCTTGTGTTCTGAACTGAGTCCCTCT 595

	Db	Accession	Source	Organism	Reference Title	Authors	Journal	Comment
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LOCUS		601507405F1	NH_MGC_71	Homo sapiens	cDNA clone IMAGE:3909192 5'			
DEFINITION		mRNA sequence.						
ACCESSION		BE885329						
VERSION		BE885329.1	GI:10334105					
KEYWORDS		EST.						
SOURCE		Homo sapiens						
ORGANISM		Homo sapiens (human)						
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.						
TITLE		1 (bases 1 to 594)						
JOURNAL		NIH-MGC http://mgc.nci.nih.gov/						
COMMENT		National Institutes of Health, Mammalian Gene Collection (MGC)						
		Unpublished						
		Contact: Robert Strausberg, Ph.D.						
		Email: ega@bsfemail.nih.gov						
		Tissue Procurement: ATCC						
		CDNA Library Preparation: Life Technologies, Inc.						
		CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)						
		DNA Sequencing by: Incyte Genomics, Inc.						
		Clone distribution: MGC clone distribution information can be						
		found through the I.M.A.G.E. Consortium/LLNL at:						
		http://image.llnl.gov						
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		High quality sequence stop: 587.						
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		/lab_host="DH10B (phage-resistant)"						
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		/note="Organ: uterus; Vector: pCMV-Sport6; Site:1; NotI;						
		Site:2; SalI; Cloned unidirectionally. Primer: Oligo dT.						
		Average insert size 2.1 kb.						
BASE COUNT		117 a 205 c 181 g 91 t						
ORIGIN								
		Query Match	87.5%	Score 560:	DB 10:	Length 594:		
		Host Local Similarity	98.3%:	Pred. No. 5.2e-106:				
		Matches 566:	Conservative 0:	Mismatches 10:	Indels 0:	Gaps 0:		
		65 CCCCAGGAGCCCCCAAAACCGTAGACATATCCCGGGGCCACAGAGCCTCGCGGCC	124					
		8 CCCCAGGAGCCCCCAAAACCGTAGACATATCCCGGGGCCACAGAGCCTCGCGGCC	67					
		QY 125 AGCCGGGCGCCGCGCATATCCCTCAGAGCGGCGCTTTCAAGCAGCGCGGAGCTTGCGCGAC	184					
		DB 68 AGCGGGGCGCCGCGCATATCCCTCAGAGCGGCGCTTTCAAGCAGCGCGGAGCTTGCGCGAC	127					
		DB 145 CGGTGTGAAGAGGTATACAGACATCCGGGAGCAGCACCCAGCAAATCCGGTGTATATC	244					
		QY 128 GCGGTGTGAAGAGGTATACAGACATCCGGGAGCAGCACCCAGCAAATCCGGTGTATATC	187					
		QY 245 GAGTCGTAACAAGGSGTAGAAGCACTGCGCTCTGAGCAAGACTAAGTTTTTGCTCCCG	304					
		DB 188 GAGCGCTAACAAAGGCTGTAAGAACACACTGCGCTCTGAGCAAGACTAAGTTTTTGCTCCCG	247					
		QY 305 GACCATTGCAACATATGAGGAGGATTTGGTCAAGATCATCCGGCGCCGCTCGACTTAACCCG	364					
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OY		365	ACGAGAGCCTTCTTCGTGGCTGGTGATCAACCAGCACAGCATAGTAGTGTTGCATTCCCGAAG	424
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OY		425	GCGGACATCTACGAGCAGAGAAABANBAGSAGSGGCTTCTCTATATGGTCTTAAGGCTACTG	484
Dd		368	GCGGACATCTACGAGCAGAGAAABANBAGSAGSGGCTTCTCTATATGGTCTTAAGGCTACTG	427
OY		485	CAGGAAMCCTTGGGCTTCTGAGGCCAGCAGTAggggaggctgcgcccttgaggaatcagaacccccc	544
Dd		428	CAGGAAMCCTTGGGCTTCTGAGGCCAGCAGTAggggaggctgcgcccttgaggaatcagaacccccc	487
OY		545	CCGGTCAGGCGCTGCCCCAGAACAGCTTGTGGTCTTCCAAGCTAGAGTGGCTTTAGGCTGGAG	604
Dd		488	CCGGTCAGGCGCTTCCCAGAACAGCTTGTGGTCTTCCAAGCTAGAGTGGCTTTAGGCTGGAG	547
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Dd		548	GCGTCGACAGCATGTGGCCGCTTACGACAGGGCA	583
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DEFINITION		AGNCOURT_6643102 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5768562		
ACCESSION		B0067721		
VERSION		B0067721.1		GI:19856767
KEYWORDS		EST.		
SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS		Mammalia; Euarchia; Primates; Catarrhini; Hominoidea; Hominids		
TITLE		NIH-MGC http://mgc.ncbi.nlm.nih.gov/		
JOURNAL		National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT		Unpublished Contact: Robert Strausberg, Ph.D. Email: rcspsr@mail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: http://image.llnl.gov/ Plate: LLML2828 row: b column: 07 High quality sequence start: 2 High quality sequence stop: 579. Location/Qualifiers 1..1281 /organism="Homo sapiens" /mol_type="mRNA" /db_xref=taxon:"9606" /cclone=IMAGE:5768502" /lab_host="DH10B" /clonetype="NH_MGC_L21" /note="Organ: brain; Vector: pCMV-Sport6; Site:1: NCBI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 26 weeks, male age 24 weeks, and male age 26 weeks. Library is oligo-dt primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by G. Gruber (Invitrogen). Research Genetics tracking code 017. Note: This is a NIH-MGC library."		
FEATURES		source		
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Best Local Similarity		98.9%	Fwd. No. 1,4e+100:	
Matches 548:		Conservative	Q: Mismatched 5:	Indels 1: gaps 1:


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DB 343 TCCCGGACCATGTCAACATGAGCAGAGTGTGTCAGATCATCCGCGCGCGCTGACAGCTGA 402
QY 360 ACCCGACGAGCGCTTCTTCTCTGCTGTGTAACACAGCAGATGTTGAGTGTCCAGCGC 419
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DB 583 GCGAGCGCGAGCTGG 596
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sequence.
ACCESSION CB111122
VERSION CB111122.1 GI:27936929
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
AUTHORS Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@email.kribd.re.kr
Plate: 8 row: G column: 02
High quality sequence stop: 560.
Location/Qualifiers
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/organism="Homo sapiens"
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/clone_11b="L5HLK1"
/note="Organ: Liver; Vector: pcnns-D2; Site_1: EcoRI;
Site_2: NotI; The poly (+) RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then deacapped
with tobacco acid pyrophosphatase (TAP). The deacapped
intact mRNA was ligated with DNA-RNA linker including
EcoRI site by treatment of T4 RNA ligase and the first
strand cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
BcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."
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BASE COUNT 113 a 199 c 166 g 82 t
ORIGIN
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Query Match 80.4%; Score 514.4; DB 14; Length 560;
Best Local Similarity 99.6%; Pred. No. 1.4e-96;
Matches 526; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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DB 33 CTCGCGACGCGCAGCCGCGCTGTCTCAGCGCGAGCCCGGAGCCCTTGAGCGCGAGCGCGC 92
QY 61 GGAG-CCCCGGAGCCCCCAACCCGACAGACATCCCCCGCGCCCGGAGCCCGCGCTGGC 119
DB 93 GGAGCCCCGGAGCCCCCAACCCGACAGACATCCCCCGCGCCCGGAGCCCGCGCTGGC 152
QY 120 GCGCCAGCGCGCGCGCGCGATGCGCTCAGACCGCGCTTCAAGCAGCGCGGAGCTTGC 179
DB 153 GCGCCAGCGCGCGCGCGCGATGCGCTCAGACCGCGCTTCAAGCAGCGCGGAGCTTGC 212
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DB 273 TCATGAGACCGCTACAAAGGTGAGAAAGCAGCTGCCGCTCTGGACAAGACCAAGTTTGG 332
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DB 333 TCCCGGACCATGTCAACATGAGCAGAGTGTGTCAGATCATCCGCGCGCGCTGACAGCTGA 392
QY 360 ACCCGACGAGCGCTTCTTCTCTGCTGTGTAACACAGCAGATGTTGAGTGTCCAGCGC 419
DB 393 ACCCGACGAGCGCTTCTTCTCTGCTGTGTAACACAGCAGATGTTGAGTGTCCAGCGC 452
QY 420 CCATGCGGACATCTACAGAGCAGAGAAAGAGAGCGCTTCTCTATATAGTCTACG 479
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DB 513 CCTCCAGGAAACCTTTCGCTTCTGAGCCAGCAGATGAGGGGGCTCGGC 560
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LOCUS B1668829
DEFINITION 603294786F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5313956 5',
mRNA sequence.
ACCESSION B1668829
VERSION B1668829.1 GI:15583062
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 15, 2003, 08:56:30 : Search time 249 Seconds
(without alignments)
5752.136 Million cell updates/sec

Title: US-09-904-603-2
Perfect score: 640
Sequence: 1 CTCGCCGAGCGCAGCGGCC.....GCCCCCTACTCAAGAGCA 640

Scoring table:
IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1504479 seqs, 118970152 residues

Total number of hits satisfying chosen parameters: 3008958

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	238.6	37.3	861	12	US-10-205-194-72
5	218.8	34.2	497	11	US-09-918-995-1874
6	215	33.6	768	14	US-10-037-270-707
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8	214.4	33.5	2199	14	US-10-277-156-3
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C 17	58.8	9.2	726	13	US-10-027-632-148570	Sequence 148570, App
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C 20	50.8	7.9	15500	9	US-09-764-869-2109	Sequence 2109, App
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C 22	50.4	7.9	3828	14	US-10-156-761-2959	Sequence 2959, App
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C 24	49.6	7.8	487	14	US-10-205-194-161	Sequence 161, App
C 25	49.2	7.7	759	10	US-09-919-580-825	Sequence 825, App
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C 27	47.2	7.4	458	11	US-09-918-995-28426	Sequence 28426, App
C 28	47.2	7.4	483	10	US-09-919-580-198	Sequence 198, App
C 29	47.2	7.4	498	14	US-10-171-581-105	Sequence 105, App
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C 31	47.2	7.4	519	10	US-09-902-941-78	Sequence 78, App
C 32	47.2	7.4	519	10	US-09-849-626-78	Sequence 78, App
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C 38	46.6	7.3	975	13	US-10-027-632-9167	Sequence 9167, App
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C 41	45.8	7.2	929	9	US-09-814-122-16	Sequence 16, App
C 42	45.6	7.1	484	11	US-09-918-995-6964	Sequence 6964, App
C 43	45.2	7.1	450	10	US-09-910-664-59	Sequence 59, App
C 44	45.2	7.1	1155	14	US-10-156-761-5751	Sequence 5751, App
C 45	45.2	7.1	9025608	14	US-10-156-761-1	Sequence 1, App

ALIGNMENTS

RESULT 1
US-09-904-603-2
Sequence 2, Appl
Publication No. US20040094612A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
GOLLY, Surya K.
TITLE OF INVENTION: N-VEL MICROTOUPLE-ASSOCIATED PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSU for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/904,603
FILING DATE: 12-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 96,749
REFERENCE/DOCKET NUMBER: PR-0211 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 640 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: JYRN0703
CLONE: 1441378
SEQUENCE DESCRIPTION: SEQ ID NO: 2
US-09-904-603-2

Query Match 100.0%; Score 640; DB 11; Length 640;
Best Local Similarity 100.0%; Pred. No. 7.6e-157;
Matches 640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-09-864-761-12594
Sequence 12594, Application US/09864761
Patent No. US2002048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeonica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
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PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
SEQ ID NO 12594
LENGTH: 570
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.66
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.66
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.65
US-09-864-761-12594

Query Match 39.9%; Score 255.2; DB 9; Length 570;
Best Local Similarity 98.8%; Pred. No. 5.7e-57;
Matches 257; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 371 CATGAGTGTGTCACGCGCCCATCGGCGCATCTAGAGAGGAGGAAAGCGGAGCG 430
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DB 431 CTTCCTATATAGTGTACGCTCCAGAAACCTTGCGGCTTGAGCCAGCAGATAGGG 490
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: CURRENT FILING DATE: 2001-07-30
: PRIOR APPLICATION NUMBER: US/09/235,076
: PRIOR FILING DATE: 1999-01-20
: NUMBER OF SEQ ID NOS: 38054
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 1874
: LENGTH: 497
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(497)
: OTHER INFORMATION: n = A,T,C or G
US-09-918-995-1874

```

```

Query Match          34.2%; Score 218.8; DB 11; Length 497;
Best Local Similarity 66.8%; Pred. No. 1.6e-47;
Matches 310; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

```

```

QY 35 CCCCCGAGCCCTTGAGCGCGAGCGCGGAGCCCGGAGCCCGCAACCGCAGACATCC 94
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 13 CCACTGAGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 72
QY 95 CCGCGCCCGCAGAGCCCGCGCTGCGCGCCCGCAGCGCGCGCGCGCGATGCTTCAGACCG 154
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 73 GGAACCTTCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 132
QY 155 CTTTGAAGGAGGCGGAGCTTCCGCGACCGCGCTGTAAGAGGTACAGACATCCGCGAC 214
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 133 ACCTTCAAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 192
QY 215 CACGACCCCGCAGAAATCCCGGTATCATGAGCGCTACAGAGGTGAGAGCGAGCTGCC 274
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 193 CACATTCACCAACAAATCCCGGTATCATGAGCGCTACAGAGGTGAGAGCGAGCTGCC 252
QY 275 GTCTTGAGAGAGCAAGTTTGTGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 334
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 253 GTTCTGATTAACAAAGTTCTTGTACCTGACCATGTCACATGATGATGATGATGATG 312
QY 335 ATCATCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 394
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 313 ATATATGAGAGGCGCTTACAGCTCATGATGATGATGATGATGATGATGATGATGATG 372
QY 395 CACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 454
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 373 CACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 432
QY 455 GACGCGCTTCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 498
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 433 GATGATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 476

```

RESULT 6

```

US-10-037-270-707
: Sequence 707, Application US/10037270
: Publication No. US20030104529A1
: GENERAL INFORMATION:
: APPLICANT: Tang, Y. Tom
: APPLICANT: Liu, Chenghua
: APPLICANT: Asundi, Vinod
: APPLICANT: Zhang, Jie
: APPLICANT: Ren, Feiyun
: APPLICANT: Chen, Rui-hong
: APPLICANT: Zhao, Qing A.
: APPLICANT: Wehrman, Tom
: APPLICANT: Xue, Aidong J.
: APPLICANT: Yang, Yonghong
: APPLICANT: Wang, Jiah-Rui
: APPLICANT: Ma, Yunqing
: APPLICANT: Wang, Dunrui
: APPLICANT: Wang, Zhiwei

```

```

: APPLICANT: Tillinghast, John
: APPLICANT: Drimanac, Radoje T.
: TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
: TITLE OF INVENTION: Polypeptides
: FILE REFERENCE: 784CIP2B
: CURRENT APPLICATION NUMBER: US/10/037,270
: CURRENT FILING DATE: 2002-01-04
: PRIOR APPLICATION NUMBER: 09/552,317
: PRIOR FILING DATE: 2000-04-25
: PRIOR APPLICATION NUMBER: 09/488,725
: PRIOR FILING DATE: 2000-01-21
: NUMBER OF SEQ ID NOS: 1104
: SOFTWARE: PL-Fl-Genes Version 1.0
: SEQ ID NO 707
: LENGTH: 768
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (109)...(486)
US-10-037-270-707

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Query Match          33.6%; Score 215; DB 14; Length 768;
Best Local Similarity 74.1%; Pred. No. 1.6e-46;
Matches 272; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

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```

QY 132 CCGCGCGATGACCTTCAGACCGCGCTTCAAGCAGCGCGGAGCTTCCGCGCGCTGTA 191
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 101 CCGCGACCATGCGCTGCGAGAAAGACCTTCAAGCAGCGCGCGCGCGCGCGCGCGCG 160
QY 192 AGAGAGTACAGCAGATCCGCGACGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 251
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 161 AAGATGTCGACATTAATTCGAGCAGCATCAACAAATCCGCGGTATGTAAGCAT 220
QY 252 ACAAGGTGAGAGCAGCTCCGCGCTTCAAGCAGCGCGCGCGCGCGCGCGCGCGCGCG 311
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 221 ACAAGGTGAGAGCAGCTTCTGTTGATTAACAAAGTCTTGTACCTGACCATG 280
QY 312 TCACATGAGCGAGTTGTCAGATCATCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 371
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 281 TCACATGAGTGAAGTATCATCAAGATTAATGAGAGGCGCTTACAGCTCATGATGATG 340
QY 372 CCTTCTCTGCTGCGAGAACCGACAGCATGATGATGATGATGATGATGATGATGATG 431
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 341 CCTTCTCTGCTGCGAGAACCGACAGCATGATGATGATGATGATGATGATGATGATG 400
QY 432 TCTACGAGCAGAGAGAGAGCAGAGCGCTTCTCTATGATGATGATGATGATGATGATG 491
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 401 TGTATGAGAGTGAAGAGATGAAGATGATGATGATGATGATGATGATGATGATGATG 460
QY 492 CCTTCGG 498
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 461 CGTTCGG 467

```

RESULT 7

```

US-09-925-301-209
: Sequence 209, Application US/09925301
: Patent No. US20020052308A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: PA106
: CURRENT APPLICATION NUMBER: US/09/925,301
: CURRENT FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCT/US00/05882
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 60/124,270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ ID NOS: 1694
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 209
: LENGTH: 2250

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: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (23)
: OTHER INFORMATION: n equals a,t,g, or c
: OS=09-925-301-209

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Query Match	33.6%	Score 215;	DB 9;	Length 2250;
Best Local Similarity	74.1%;	Pred. NO. 1.7e-46;		
Matches 272;	Conservative	0;	Mismatches 95;	Indels 0;
				Gaps 0;

QY	132	CCGCGGGAGTCCCTCAGACCGGCGCTTTCAAGCAGCGCGGAGGTTGGTCGACCGCTTA	191
Db	158	CCCGCAACCAATDCCGTGCGAAGAACCTTTCAAGCAGCGCGGACCTTCGACCAAGAGTAGT	217
QY	192	AGGAGGTACACACAGATCCGGGACCGACGACCCCGACCAAAATCCCGGTGA	251
Db	218	AAGATGTCCGCACTATTATTCGAGAGGACGATCCAAACCAAAATCCCGGTGATATAGAACAT	277
QY	252	ACAAGGGTGAAGACAGTGGCGGCTCTGTGACAAAGATCCAAAGTTTGTGCCGAGCATG	311
Db	278	ACAAGGGTGAAGAACAGCTTCTCTTGTGGATAAACAAAGCTCTTGACTGGACGATG	337
QY	312	TCACATGAGGAGTGTGGTCAAGATTCATCCGGCGCGGCTGACGTGAAGCCGACGCGAGG	371
Db	338	TCACATGAGTGAAGCTCATCAAGATTAATTACAAAGCGGCTTACAGTTCAAATGCTAATTCAGG	397
QY	372	CCTTCTTCCTGCTGGTGAACCCAGCAGCATGTGTAGTGTGTGCACGGCCATCCGGGACGA	431
Db	398	CCTTCTTCCTGTTGGTGAACCGGACACAGCATGTGTAGGTTCTCAGACCAATCTTAGAGG	457
QY	432	TCTAGCAGCAGGAGAAAGACGAGGACGGCTTCTCTATATGTGTACGGTCTCCAGGAAA	491
Db	458	TGATGACAGGTGAAGAAAGATGAAGATGGATTCTGTACATGCTGTATCCCTCCGAGAGA	517
QY	492	CCTTCGG 498	
Db	518	CGTTGG 524	

```

RESULT 8
US-10-277-156-3
: Sequence 3, Application US/10277156
: Publication No. US20030054399A1
: GENERAL INFORMATION:
: APPLICANT: LADONGA et al.
: TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
: TITLE OF INVENTION: USES THEREOF
: FILE REFERENCE: CLO00842 DIV
: CURRENT APPLICATION NUMBER: US/10/277,156
: CURRENT FILING DATE: 2002-10-22
: PRIOR APPLICATION NUMBER: 09/7708,725
: PRIOR FILING DATE: 2000-11-09
: PRIOR APPLICATION NUMBER: 60/243,428
: PRIOR FILING DATE: 2000-10-27
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 3
: LENGTH: 2199
: TYPE: DNA
: ORGANISM: Human
: US-10-277-156-3

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	Query Match	Score	214.4	DB	14	Length	2159
	Best Local Similarity	68.5%	Pred.	2.5e-46			
	Matches	296	Conservative	0	Mismatches	136	Indels
							Gaps
0Y	67	CCGAGAGCCCCAAACCGGACGACATCCCGCGGCCCCGAGAGCCCGCGGCTTGGCGGCCCGAC	126				
0b	750	CCGAGGAGAGCGCCGACACCCCGAGGAGCGCGCGGAGACCTCGGATGTCGCGCGCGCGGCC	809				

QY	127	CGGGGCGCGGCGGATGGCGTTCAGAGCGGGCTTTGAAACAGCGGGGAGAGCTTCGCGTAAAG	366
Db	810	AGATGCTCCACACCATGCGGTGGGGAACGCTTTAAACACGCGCGCACGCTTCGAACTAAAG	869
QY	187	CTGTAAAGAGATATACACAGATCCGCGGATATACATCCCGAGCAAAATCCCGGCGATATATA	246
Db	870	AGTGAAGATGTGGACTTATATGAAAGGAGCATGCAACCAAAATCCGCGGATATATA	924
QY	247	GCGCTACAAAGGTGAGAGAGCAGCTGGCGGCTGCTGGACAGACCAAGTTTTCGTTGCGGA	306
Db	930	ACGATACAAAGGTGAGAGAGCAGCTTCCTGTTTCGATATAAACAAGATTCCTTGGATCTGA	989
QY	307	CCATGTCACATGAGCGAGTTGGTCAGATCATCGCGCGCGCTGAGCGCTGAACCTCCAG	366
Db	990	CCATGTCACATGAGTGAAGCTCATCAAGATATATAGAAAGCGCTTATAGGTTCAATGCTTAA	1049
QY	367	GCAGCGCTTCCTTCGTTGAGAACATACAGATAGTGAAGTGTGCAATATATATATAT	426
Db	1050	TCAGCGCTTCCTTCGTTGAGAACATATATATATATATATATATATATATATATATATAT	1109
QY	427	GGACATCTACCAAGAGCAAAAGACAGATGCTTCGCTATATATGTTATATGTTATATATA	486
Db	1110	AGAGGTCATAGCAGAGTGAAGAAAGATGAAGATGCTTCGCTATATGTTATATGTTATATATA	1169
QY	487	GGAACCTTCGG	498
Db	1170	GGAGACGTTGG	1181

```

1 RESULT 9
2 US-09-917-800A-1201/c
3 ; Sequence 1201, Application US/09917860A
4 ; Patent No. US20020119462A1
5 ; GENERAL INFORMATION:
6 ; APPLICANT: Mendrick, Donna
7 ; APPLICANT: Porter, Mark
8 ; APPLICANT: Johnson, Kory
9 ; APPLICANT: Castle, Arthur
10 ; APPLICANT: Elashoff, Michael
11 ; APPLICANT: Gene Logic, Inc.
12 ; TITLE OF INVENTION: Molecular Toxicology Modeling
13 ; FILE REFERENCE: 44921-5038-US
14 ; CURRENT APPLICATION NUMBER: US/09/917,800A
15 ; CURRENT FILING DATE: 2001-07-31
16 ; PRIOR APPLICATION NUMBER: US 60/222,040
17 ; PRIOR FILING DATE: 2000-07-31
18 ; PRIOR APPLICATION NUMBER: US 60/222,880
19 ; PRIOR FILING DATE: 2000-11-02
20 ; PRIOR APPLICATION NUMBER: US 60/290,029
21 ; PRIOR FILING DATE: 2001-05-11
22 ; PRIOR APPLICATION NUMBER: US 60/290,645
23 ; PRIOR FILING DATE: 2001-05-15
24 ; PRIOR APPLICATION NUMBER: US 60/292,346
25 ; PRIOR FILING DATE: 2001-05-22
26 ; PRIOR APPLICATION NUMBER: US 60/295,768
27 ; PRIOR FILING DATE: 2001-06-06
28 ; PRIOR APPLICATION NUMBER: US 60/297,457
29 ; PRIOR FILING DATE: 2001-06-13
30 ; PRIOR APPLICATION NUMBER: US 60/298,884
31 ; PRIOR FILING DATE: 2001-06-19
32 ; PRIOR APPLICATION NUMBER: US 60/303,459
33 ; PRIOR FILING DATE: 2001-07-09
34 ; NUMBER OF SEQ ID NOS: 1740
35 ; SOFTWARE: PatentIn Ver. 2.1
36 ; SEQ ID NO 1201

```

Query Match 30.18; Score 192.4; DB 10; Length 547;

Db 121 GAGAGTGAAGAGATGATGATCTCTGATACGTCTGTGGCTTCCAGGAGCGTTTC 180
QY 497 GG 498
Db 181 GG 182

RESULT 12
US-09-864-761-885/c
Sequence 885, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 885
LENGTH: 474
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL078644.10
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.9
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.93

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3
US-09-864-761-885

Query Match 14.9%; Score 95.6; DB 9; Length 474;
Best Local Similarity 65.4%; Pred. No. 1,5e-15;
Matches 140; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 261 AGAGCAGCTGCCGTCTCTGACAGACAGCTTTTGGTCGAGCATGTCAGATGATGA 420
Db 474 AAAGCAGCTTCGTCTCTGAGAAAACAGATTTTGTACGTGATGATGATGAATGA 415
QY 321 GCGAGTTGGTCAAGATGATGAGCGGCTTGCAGCTGAACCCGACGAGGAGCTTGTTC 480
Db 414 GTAACTGTCAGATGATTTAGAAAGCCCTTAAAGCTGATAGTATGATGATGATGAT 455
QY 381 TGCTGTGACACAGACAGCATGATGATGATGATGATGATGATGATGATGATGAT 440
Db 354 TAGTGTGAGCAGACAGACAGCTTGTGAGATTTTCATGCTGATGATGATGATGATG 495
QY 441 AGAGAAAGACAGAGAGCGGCTTCTGATATGCT 474
Db 294 GTGAGAGAGATGAGAGAGATTTCTGATGAT 261

RESULT 13
US-09-864-761-17665/c
Sequence 17665, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 885
LENGTH: 474
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL078644.10
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.9
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.93

;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO: 17665
;; LENGTH: 155
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AL078644.10
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.9
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.93
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3
;; OTHER INFORMATION: NT HIT: U80885.1, EVALUE 2.00e-11
;; OTHER INFORMATION: SWISSPROT HIT: O41515, EVALUE 2.00e-10
;; OTHER INFORMATION: EST_HUMAN HIT: AA723823.1, EVALUE 3.00e-72
US-09-864-761-17665

Query Match 11.2%; Score 71.4; DB 9; Length 155;
Best Local Similarity 66.7%; Pred. No. 2.7e-09;
Matches 102; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 267 AGCTGCGGCTCTGACACAGCAAGTTTGTGTCGCGGACCATGTCAATGAGCGAGT 326
DB 155 AGCTTCTGCTCTGAAAAACCAAGTAATTTGTACATGATCAAGTCAACATGAGTAAC 96
QY 327 TGTCAAGATCATCGGCGCGCTGCAGCTGAACCCGACGAGCTTTCTTCTGCTGG 386
DB 95 TCGTCAATATATTAGAGGCGCTTAAGCTCGATAGTAATCAAGCCCTTCTTCTAGTGG 36
QY 387 TGAACGACGACGATGCTGAGTGTGTCACGC 419
DB 35 TGACGACGACGAGCTTGGTGTGATTTTCCATGC 3

RESULT 14
US-09-917-800A-1711
;; Sequence 1711, Application US/09917800A
;; Patent No. US20020119462A1
;; GENERAL INFORMATION:
;; APPLICANT: Mendrick, Donna
;; APPLICANT: Porter, Mark
;; APPLICANT: Johnson, Kory
;; APPLICANT: Castle, Arthur
;; APPLICANT: Elashoff, Michael
;; APPLICANT: Gene Logic, Inc.
;; TITLE OF INVENTION: Molecular Toxicology Modeling
;; FILE REFERENCE: 44921-5038-US
;; CURRENT FILING DATE: 2001-07-31
;; PRIOR APPLICATION NUMBER: US/09/917,800A
;; PRIOR FILING DATE: 2000-07-31
;; PRIOR APPLICATION NUMBER: US 60/222,880
;; PRIOR FILING DATE: 2000-11-02
;; PRIOR APPLICATION NUMBER: US 60/290,029
;; PRIOR FILING DATE: 2001-05-11
;; PRIOR APPLICATION NUMBER: US 60/290,645
;; PRIOR FILING DATE: 2001-05-15
;; PRIOR APPLICATION NUMBER: US 60/292,336
;; PRIOR FILING DATE: 2001-05-22
;; PRIOR APPLICATION NUMBER: US 60/295,798
;; PRIOR FILING DATE: 2001-06-06
;; PRIOR APPLICATION NUMBER: US 60/297,457
;; PRIOR FILING DATE: 2001-06-13
;; PRIOR APPLICATION NUMBER: US 60/298,884

;; PRIOR FILING DATE: 2001-06-19
;; PRIOR APPLICATION NUMBER: US 60/303,459
;; PRIOR FILING DATE: 2001-07-09
;; NUMBER OF SEQ ID NOS: 1740
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 1711
;; LENGTH: 975
;; TYPE: DNA
;; ORGANISM: Rattus norvegicus
;; FEATURE:
;; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_022706
US-09-917-800A-1711

Query Match 11.2%; Score 71.4; DB 10; Length 975;
Best Local Similarity 51.6%; Pred. No. 3e-09;
Matches 215; Conservative 0; Mismatches 196; Indels 6; Gaps 2;

QY 92 TCCCGCGCCCGACAGCCCGGCTGCGCGCCCGACCGCGCGCGCATGCGTCAGAC 151
DB 53 TCGCTTCCCGCAAGTCTGCGGCTCAAGAGCGCGCTCCGCTTCCCGCGCATGAAG 112
QY 152 CGGCTTTCAGACGCGCGGAGCTTCCCGCGCGCGCTGTAAGAGAGTACAGATCCGC 211
DB 113 TGGATGTTTAAAGAGGACCACTGCTGGAACACAGATCGTGAATCCGGAAGATCAGA 172
QY 212 GACGACAGCCCGACGAAATCCCGGTGATCATCGAGCCCTACAGGAGTGAAGACGCTG 271
DB 173 GCGAATATCCCGGACCGGCTTCCGCTGATCGTTGAG---AAGTCTCGCTTCAGATT 229
QY 272 CCGCTTCTGACACAGCAAGTTTGTGTCGCGGACCATGTCACATGAGGATGCTG 331
DB 230 GTTGACATTGACAAAGAGAGTACTTGTCCATCTGACATCAGTGTGCTCAGTTCAATG 289
QY 332 AAGATCATCGGCGCGCTGAGCTGAACCCGACGAGCGCTTCTGCTGCTGAGAC 391
DB 290 TGGATCATCAGAAAGAGATCCAGCTTCTTCTGAGAGGCGATCTTCTGTTGTGAGAC 349
QY 392 CAGCAGACATGTTGAGTGTTCACGCCCATTCGCGGAGCATCTACAGACGAGAAAGAC 451
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DB 407 GAAGATGATTTCTGTATGTGCGCTACACGAGAGAACTTTGGCTTGTGAGCC 463

RESULT 15
US-10-205-342-24
;; Sequence 24, Application US/10205342
;; Publication No. US20030108906A1
;; GENERAL INFORMATION:
;; APPLICANT: Warner-Lambert Company
;; APPLICANT: Lee, Kevin
;; APPLICANT: Dixon, Alstair
;; APPLICANT: Brookspank, Robert
;; APPLICANT: Pinnock, Robert
;; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
;; FILE REFERENCE: WL-A-018198
;; CURRENT APPLICATION NUMBER: US/10/205,342
;; PRIOR FILING DATE: 2002-07-24
;; PRIOR APPLICATION NUMBER: GB 0118354.0
;; PRIOR FILING DATE: 2001-07-27
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO: 24
;; LENGTH: 975
;; TYPE: DNA
;; ORGANISM: Rattus norvegicus
;; FEATURE:
;; OTHER INFORMATION: cDNA: Ganglioside expression factor 2
US-10-205-342-24

Query Match 11.2%; Score 71.4; DB 14; Length 975;

Best Local Similarity 51.6%; Pred. No. 3e-09;
Matches 215; Conservative 0; Mismatches 196; Indels 6; Gaps 2;

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QY 332 AAGATCATCCGCGCGGCTGAGCTGAACCCACGCGAGGCGTCTTCTGCTGTGAG 391
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QY 452 GAGGACGCTTCTCTATATGCTACGCTTCCAGAAACCTTGCGTTCTGAGGC 508
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Db 407 GAAGATGATTTCTGTATGTGGCTACAGCGAGAGAACCTTTGGCTTCTGAGCC 463
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Job time : 259 secs

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